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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1496.84 Seconds

(Without alignments)
10479.665 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggaccagagacccttcgag.....agtaaacattcccggaattcc 539

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*
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40: gb_ov:*
41: gb_ov:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	539	100.0	539 6 AX147744	AX147744 Sequence
2	539	100.0	539 6 AX300781	AX300781 Sequence
3	539	99.4	710 10 RATIGFIA	M15480 Rat Insulin
4	516.6	95.8	798 10 RNIGF12	X05108 Rat mRNA (c
5	516.6	95.8	958 10 RNIGF12	X05107 Rat mRNA (c
6	470.2	87.2	1536 10 BC012409	BC012409 Mus muscu
7	453.8	84.2	651 10 MMIGFIBR	X04482 Mouse mRNA
8	425	78.8	487 6 AX147752	AX147752 Sequence
9	425	78.8	487 6 AX300789	AX300789 Sequence
10	421.8	78.3	1346 10 RATIGFIB	M15481 Rat Insulin
11	402.6	74.7	1052 10 RATIGFIA	D00698 Rattus sp.
12	401	74.4	513 10 RATGJIL	M17714 Rat Insulin
13	387	71.8	826 10 RATIGFIA	X06043 Rat mRNA fo
14	361.6	67.1	696 10 MMIGFIA	M17335 Rat Insulin
15	361.6	66.2	523 6 AX147746	X04480 Mouse mRNA
16	356.8	66.2	523 6 AX300783	AX147746 Sequence
17	356.8	66.2	523 6 AX300783	AX300783 Sequence
18	325.2	60.3	517 6 AX147742	AX147742 Sequence
19	325.2	60.3	517 6 AX300779	AX300779 Sequence
20	274.2	50.9	7260 6 AX375028	AX375028 Sequence
21	274.2	50.9	7260 6 AX411095	AX411095 Sequence
22	274.2	50.9	7260 6 HSIGFACI	X57025 Human IGF-I
23	272.6	50.6	666 6 A29119	A29119 H.sapiens I
24	272.6	50.6	725 6 HSIGF1	X00173 Homo sapien
25	272.6	50.6	728 6 HUMGRII	M29644 Human Insul
26	271.2	50.3	616 6 HSIGF1A	X56773 H.sapiens m
27	271.2	50.3	620 6 HSIGF1A	X08370 Sequence 2
28	270	50.1	1076 6 HUMIGFI	M27544 Human Insul
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30	267.2	49.6	432 4 AF022961	AF022961 Oryctolag
31	262	48.6	471 6 AX147754	AX147754 Sequence
32	262	48.6	471 6 AX300791	AX300791 Sequence
33	260	48.2	567 6 PIIGFRIA	M31175 Pig Insulin
34	258	47.9	532 4 SSIGFIM	X17492 Porcine mRN
35	237.4	44.0	888 4 ECUS5272	U85272 Equus cabal
36	231	42.9	730 9 HSIGFIB	X56774 H.sapiens m
37	231	42.9	1094 9 HUMGRIIB	M11568 Human Insul
38	231	42.9	1136 6 E01349	E01349 CDNA encodi
39	231	42.9	1136 6 I08009	I08009 Sequence 3
40	230.2	42.7	978 4 GOTIGFI	D11378 Goat mRNA f
41	230.2	42.7	978 6 B05279	B05279 DNA encodin
42	228.6	42.4	836 10 AF440694	AF440694 Mus muscu
43	228.6	42.4	836 10 CP1GFI	X52851 Guinea pig
44	228.6	42.4	1284 4 B11GFI	X15726 Bovine mRNA
45	224	41.6	612 9 HUMIGFIB	M37484 Human Insul

ALIGNMENTS

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RESULT 1
AX147744
LOCUS AX147744 539 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136483.
ACCESSION AX147744
VERSION AX147744.1 GI:14346789
KEYWORDS
SOURCE
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 539)
AUTHORS Goldspink, G.R. and Johnson, I.R.
TITLE Use of the insulin-like-growth factor 1 isoform mgf for the
```

Pred. No. is the number of results predicted by chance to have a

JOURNAL
treatment of neurological disorders
Patent: WO 0136483-A 3 25-MAY-2001;
University College London (GB)

FEATURES

Location/Qualifiers
1..539

CDS

/organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1..336
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC41176.1"
/db_xref="GI:14346790"
/translation="GPEPLCGAEVLDALQFVCGPRGFENKPTVYGSIRAPDTGIV
DECCFRSCDLRLRLMVCVRCFKTSARSIRARHDMPTKQSPSTLTHKKRLQRRR
KSTLEERK"

BASE COUNT

161 a 136 c 139 g 103 t

ORIGIN

Query Match 100.0%; Score 539; DB 6; Length 539;
Best Local Similarity 100.0%; Pred. No. 9.2e-159; Indels 0; Gaps 0;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACAGAGACCCCTTGGCGGGCTGAGCTGTGAGAGCTCTTCACTTGTGTGACCA 60
DB 1 GGACAGAGACCCCTTGGCGGGCTGAGCTGTGAGAGCTCTTCACTTGTGTGACCA 60
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DB 61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACAG 120
QY 121 ACGGGCAATGTGATGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB 121 ACGGGCAATGTGATGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
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QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATCGACACACAAGAAAGAAAGCTGCAAGG 300
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QY 361 CAGAATGTAGAGAGAGCTCCGAGAGACAGAAAATGCCACGCCAAGATCCTTTG 420
DB 361 CAGAATGTAGAGAGAGCTCCGAGAGACAGAAAATGCCACGCCAAGATCCTTTG 420
QY 421 CTGCTTGAGCAACCTGCAAAACATGGAGACACCTGCCAATATCAATATAGTTGATA 480
DB 421 CTGCTTGAGCAACCTGCAAAACATGGAGACACCTGCCAATATCAATATAGTTGATA 480
QY 481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATAACAAAGTAACATTCGCGAATTC 539
DB 481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATAACAAAGTAACATTCGCGAATTC 539

RESULT 2

AX300781 539 bp DNA linear PAT 30-NOV-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0185781.
ACCESSION AX300781
VERSION AX300781.1 GI:17382062
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage
JOURNAL Patent: WO 0185781-A 3 15-NOV-2001;
University College London (GB); East Grinstead Medical Research
Trust (GB)

FEATURES

Location/Qualifiers
1..539

CDS

/organism="Rattus sp."
/db_xref="taxon:10118"
<1..336
/note="unnamed protein product"
/codon_start=1
/protein_id="Cadi3041.1"
/db_xref="GI:17382063"
/translation="GPEPLCGAEVLDALQFVCGPRGFENKPTVYGSIRAPDTGIV
DECCFRSCDLRLRLMVCVRCFKTSARSIRARHDMPTKQSPSTLTHKKRLQRRR
KSTLEERK"

BASE COUNT

161 a 136 c 139 g 103 t

ORIGIN

Query Match 100.0%; Score 539; DB 6; Length 539;
Best Local Similarity 100.0%; Pred. No. 9.2e-159; Indels 0; Gaps 0;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACAGAGACCCCTTGGCGGGCTGAGCTGTGAGAGCTCTTCACTTGTGTGACCA 60
DB 1 GGACAGAGACCCCTTGGCGGGCTGAGCTGTGAGAGCTCTTCACTTGTGTGACCA 60
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACAG 120
DB 61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACAG 120
QY 121 ACGGGCAATGTGATGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB 121 ACGGGCAATGTGATGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
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DB 181 TGTGTCGGCTGCAAGCTCAAAAGTCAGTGTGCTTCCATCCGGCCGACGACACTGAC 240
QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATCGACACACAAGAAAGAAAGCTGCAAGG 300
DB 241 ATGCCCAAGACTCAGAGTCCAGCCCTATCGACACACAAGAAAGAAAGCTGCAAGG 300
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DB 301 AGAAGAAAGAAAGTCACTTGAAGACACAGTGAAGAGTGAAGAAACAGACCTA 360
QY 361 CAGAATGTAGAGAGAGCTCCGAGAGACAGAAAATGCCACGCCAAGATCCTTTG 420
DB 361 CAGAATGTAGAGAGAGCTCCGAGAGACAGAAAATGCCACGCCAAGATCCTTTG 420
QY 421 CTGCTTGAGCAACCTGCAAAACATGGAGACACCTGCCAATATCAATATAGTTGATA 480
DB 421 CTGCTTGAGCAACCTGCAAAACATGGAGACACCTGCCAATATCAATATAGTTGATA 480
QY 481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATAACAAAGTAACATTCGCGAATTC 539
DB 481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATAACAAAGTAACATTCGCGAATTC 539

RESULT 3

RATIGFIA 710 bp mRNA linear ROD 27-APR-1993
LOCUS
DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION M15480
VERSION M15480.1 GI:204749
KEYWORDS
SOURCE Rat (Sprague-Dawley) adult liver cDNA to mRNA, clone pRIGF-1-42.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 710)

AUTHORS Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and Lebois,D.

TITLE Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahepatic tissues

JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)

MEDLINE 88288198

PUBMED 3453891

COMMENT Draft entry and computer-readable copy of sequence in [MO]. Endocrinol. (1987) in press kindly provided by S.R.Lasky, 16-Mar-1987.

FEATURES Location/Qualifiers

source 1..710

organism="Rattus norvegicus"

db_xref="taxon:10116"

cds 106..507

/note="insulin-like growth factor precursor"

/codon_start=1

/protein_id="AA041385.1"

/db_xref="GI:204750"

/translation="MSSSLFLVLAQLLFTSSATAPETLGAELVDALQVCGPRG FYNKPTGYGSSIRAPQGIYDECCFRSCDLRLKEMVCVRCKPTKSARSIRARHTD MPKTKSOPLSHKKRKLQRRKSTLEBK"

106..171

/note="insulin-like growth factor signal peptide"

172..258

/product="insulin-like growth factor B peptide"

259..294

/product="insulin-like growth factor C peptide"

295..357

/product="insulin-like growth factor A peptide"

358..381

/product="insulin-like growth factor D peptide"

382..504

/product="insulin-like growth factor E peptide"

BASE COUNT 202 a 191 c 172 g 145 t

ORIGIN 1 bp upstream of EcoRI site.

Query Match 99.4%: Score 535.8; DB 10; Length 710; Best Local Similarity 99.6%; Pred. No. 9e-158; Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTCGCGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 60

DB 172 GGACCAAGACCCCTTCGCGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 231

QY 61 AGGGCTTTTACTTCAACAAGCCCAAGTATGCTGCTGAGCTGAGGACACACAG 120

DB 232 AGGGCTTTTACTTCAACAAGCCCAAGTATGCTGCTGAGCTGAGGACACACAG 291

QY 121 ACGGCAATGTGATGAGTGTGCTTCGAGCTGTGATGTGAGAGCTGAGATGAC 180

DB 292 ACGGCAATGTGATGAGTGTGCTTCGAGCTGTGATGTGAGAGCTGAGATGAC 351

QY 181 TGTTCGCTGCAAGCTTCAAGATCAGTGTTCATCCGAGCCAGGACACACTGAC 240

DB 352 TGTTCGCTGCAAGCTTCAAGATCAGTGTTCATCCGAGCCAGGACACACTGAC 411

QY 241 ATGCCCAAGACTGGAAGTCCGACCCCTATGCACACAAAGAAAGAACTGCAAG 300

DB 412 ATGCCCAAGACTGGAAGTCCGACCCCTATGCACACAAAGAAAGAACTGCAAG 471

QY 301 AGAAGGAAGAAATACCTTGAAGAACACAAAGTGAAGAGTGAAGAAAGACCTA 360

DB 472 AGAAGGAAGAAATACCTTGAAGAACACAAAGTGAAGAGTGAAGAAAGACCTA 531

QY 361 CAGATATGAGAGAGAGCTCCCGAGGAAAGAAATGCGACCTACCGCAAGTCTTG 420

DB 532 CAGATATGAGAGAGAGCTCCCGAGGAAAGAAATGCGACCTACCGCAAGTCTTG 591

QY 421 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAATATCAATATGAGTTCA 480

DB 592 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAATATCAATATGAGTTCA 651

QY 481 TCATTAGAGATGGGCAATTCCTCCATGAAGTAATACAGTAACATTCCTCCGGAATTC 539

DB 652 CCATTGAGAGATGGGCAATTCCTCCATGAAGTAATACAGTAACATTCCTCCGGAATTC 710

RESULT 4

RNIF12 798 bp mRNA linear ROD 12-SEP-1993

LOCUS Rat mRNA (clone IGf1a2) for Insulin-like growth factor I.

DEFINITION X06108 M2339 J00429

ACCESSION X06108.1 GI:56426

VERSION Insulin-like growth factor I.

KEYWORDS Rattus norvegicus.

SOURCE Rattus norvegicus.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 798)

AUTHORS Rotwein,P.

TITLE Direct Submision

JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO 63110, USA

2 (bases 1 to 798)

AUTHORS Shimatsu,A. and Rotwein,P.

TITLE Sequence of two Rat Insulin-like Growth Factor I mRNAs Differing Within the 5' Untranslated Region

JOURNAL Nucleic Acids Res. 15 (1987) in press

COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is described in <X06107>.

FEATURES Location/Qualifiers

source 1..798

organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/tissue_type="liver"

1..72

/note="5' UT-region"

73..552

/note="IGF-I (AA 1-159)"

/codon_start=1

/protein_id="CA029481.1"

/db_xref="GI:56427"

/translation="MGKISSLPVLEKICLDFKIRIHMSHFLVLAQLLFTS SATAGBELGALVDALQVCGPRGFYFNKPTGYGSSIRAPQGIYDECCFRSCDL RLKEMVCVRCKPTKSARSIRARHTDMPKTKSOPLSHKKRKLQRRKSTLEBK"

553..798

/note="3' UT-region"

BASE COUNT 238 a 196 c 183 g 181 t

ORIGIN

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QY 1 GGACCAAGACCCCTTCGCGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 60

DB 217 GGACCAAGACCCCTTCGCGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 276

QY 61 AGGGCTTTTACTTCAACAAGCCCAAGTATGCTGCTGAGCTGAGGACACACAG 120

DB 277 AGGGCTTTTACTTCAACAAGCCCAAGTATGCTGCTGAGCTGAGGACACACAG 336

QY 121 ACGGCAATGTGATGAGTGTGCTTCGAGCTGTGATGTGAGAGCTGAGATGAC 180

DB 337 ACGGCAATGTGATGAGTGTGCTTCGAGCTGTGATGTGAGAGCTGAGATGAC 396

QY 181 TGTTCGCTGCAAGCTTCAAGATCAGTGTTCATCCGAGCCAGGACCAACTGAC 240

DB 397 TGTTCGCTGCAAGCTTCAAGATCAGTGTTCATCCGAGCCAGGACCAACTGAC 456

QY 241 ATGCCCAAGACTGGAAGTCCGACCCCTATGCACACAAAGAAAGAAAGTGAAG 300

Db 457 ATGCCAAGACTCAGAGTCCAGCCCTATGCACACACAGAAAGAACCTCCAAAGG 516
 QY 301 AGAAGAAAGAAAGTACACTTAAAGACACAGTGAAGTGCAGAAACAGACCTA 360
 Db 517 AGAAGAAAGAAAGTACACTTAAAGACACAGTGAAGTGCAGAAACAGACCTA 576
 QY 361 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACGTACCGCAAGATCTTGG 420
 Db 577 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACGTACCGCAAGATCTTGG 636
 QY 421 CTGCTTGAGAGACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 480
 Db 637 CTGCTTGAGAGACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 696
 QY 481 TCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAAACATTC 531
 Db 697 CCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAAACATTC 747

RESULT 5
 LOCUS ENIGFI1 958 bp mRNA linear ROD 12-SEP-1993
 DEFINITION Rat mRNA (clone IGFIAB1) for insulin-like growth factor I.
 ACCESSION X06107 M32260 Y00429
 VERSION X06107.1 GI:56424
 KEYWORDS insulin-like growth factor I.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 958)
 AUTHORS Rotwein, P.
 TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO 63110, USA

REFERENCE 2 (bases 1 to 958)
 AUTHORS Shimatsu, A. and Rotwein, P.
 TITLE Sequence of two rat insulin-like growth factor I mRNAs differing within the 5' untranslated region
 JOURNAL Nucleic Acids Res. 15 (17), 7196 (1987)
 MEDLINE 88015572
 PUBMED 3658684

COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is described in <X06108>.

FEATURES
 source location/Qualifiers

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 /strain="Sprague-Dawley"
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 CDS 259..738
 /note="IGF-I (AA 1-159)"
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 /protein_id="CAA29480.1"
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 /translation="MKTISLPTQLFKICLDFLTKIKHMSSTLPLALCLTFTS
 SAVAGEPLCGAEVLDAIOFVCGPRGFYFNKPTGYGSSIRAPDTGIVDECCFRSCDL
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 /note="3' UT-region"
 misc_feature 260 a 246 c 209 g 243 t

BASE COUNT 260 a 246 c 209 g 243 t
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Query Match 95.8%; Score 516.6; DB 10; Length 958;
 Best Local Similarity 98.3%; P-Id. No. 1.2e-151;
 Matches 522; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGACGAGAGACCTTGGGGGAGCTGAGCTGGTGAAGCTCTTCAGTGTGTGACCA 60
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 QY 61 AGGGCTTTACTTACACAGCCACAGCTATATGAGCTCCAGCATTCGGAGGCGACCAAG 120
 Db 463 AGGGCTTTACTTACACAGCCACAGCTATATGAGCTCCAGCATTCGGAGGCGACCAAG 522
 QY 121 AGGGCATTTGATGATGAGTGTGCTTCGGGAGCTGTATCTGAGAGAGCTGAGATGTAC 180
 Db 523 AGGGCATTTGATGATGAGTGTGCTTCGGGAGCTGTATCTGAGAGAGCTGAGATGTAC 582
 QY 181 TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCTACCTGAC 240
 Db 583 TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCTACCTGAC 642
 QY 241 ATGCCCAAGACTCAGAGTCCCGAGCCCTATGACACACAGAAAGAGAGCTCAAGG 300
 Db 643 ATGCCCAAGACTCAGAGTCCCGAGCCCTATGACACACAGAAAGAGAGCTCAAGG 702
 QY 301 AGAAGAAAGAAAGTACACTTGAAGACACAGTGAAGAGTGCAGAAACAGACCTA 360
 Db 703 AGAAGAAAGAAAGTACACTTGAAGACACAGTGAAGAGTGCAGAAACAGACCTA 762
 QY 361 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACGTACCGCAAGATCTTGG 420
 Db 763 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACGTACCGCAAGATCTTGG 822
 QY 421 CTGCTTGAGAGACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 480
 Db 823 CTGCTTGAGAGACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 882
 QY 481 TCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAAACATTC 531
 Db 883 CCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAAACATTC 933

RESULT 6
 LOCUS BC012409 1536 bp mRNA linear ROD 07-AUG-2002
 DEFINITION Mus musculus, Similar to Insulin-like growth factor 1, clone
 ACCESSION BC012409
 VERSION BC012409.1 GI:15214568
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1536)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://imgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcabs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Guarante: P.H. Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 24 Row: k Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6754307
Location/Qualifiers

CDS

BASE COUNT	485 a	324 c	303 g	424 t
ORIGIN				

Query Match	87.2%	Score 470.2;	DB 10;	Length 1536;
Best Local Similarity	92.8%;	Pred. No. 5.9e-137;		
Matches 493;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;

RESULT 7	MMISF1BR	LOCUS	DEFINITION
	MMIGF1BR	651 bp	linear
		Mouse mRNA for preproinsulin-like growth factor IB.	ROD 21-MAR-1995

SOURCE	Mus musculus.
ORGANISM	Mus musculus
REFERENCE	Etkayeva; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus: I. (Phase I to 651)
AUTHORS	Bell G.I., Stempien M.M., Fong N.M. and Ball L.B.
TITLE	Sequences of liver cDNAs encoding two different mouse insulin-like growth factor I precursors
JOURNAL	Nucleic Acids Res. 14 (20), 7873-7882 (1986)
MEDLINE	87040760
PUBMED	3774549
COMMENT	The sequence is identical to the preproIGF-IA sequence (X04480) except for the presence of a 52 bp insertion following codon 86 (position 397 to 448), caused by alternative RNA splicing. The B domain of IGF comprises residues 1-29 (position 139-225), the C domain residues 30-41 (position 226-261), the A domain residues 42-62 (position 262-324) and the D domain residues 63-70 (position 325-348).
FEATURES	location/Qualifiers
SOURCE	1..651

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misc_feature      /tissue_type="liver"
                  43..45
                  /note="pot. translation start"
CDS               73..474
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                  /protein_id="CAA28170.1"
                  /db_xref="GI:51807"
                  /db_xref="MGD:MG1:96432"
                  /db_xref="SWISS-PROT:P05018"
                  /translation="MSSSHYFETALCLPTFSSMTAPENICGAELYPALDPCVCPRR
FENKPLPGHSSLRAPQGLYDECCFSCDLDRELENYCAPLPTAAASINAGSHHT
MPKIQSPSLSTKTKTKLQRRKGSFEEK"
sig_peptide       73..138
mat_peptide       139..348
misc_feature      /product="mature IGF-1B (aa 1-70)"
                  349..471
                  /note="COOH-terminal peptide (E domain) (aa 71 to 111)"
polya_site        651
                  /note="polyA site"
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Query Match	84.2%	Score 453.8	DB 10	Length 651
Best Local Similarity	92.8%	Pred. No. 7.5e-132		
Matches 476	Conservative 0	Mismatches 37	Indels 0	Gaps 0
QY	1	GGACCAAGACGCTTTGCGGGCTGAGCTGATGAGACGCTTTCAGTGTGTGTGGACCA	60	
Db	139	GGACCAAGAGCCCTTTGCGGGCTGAGCTGATGAGACGCTTTCAGTGTGTGTGGACCG	198	
QY	61	AGAGGCGTTTACTTCAACAAGCCACAGCTGTGAGCTTCACATTCGAGAGGACCCACAG	120	
Db	199	AGAGGCGTTTACTTCAACAAGCCACAGGCTGTGAGCTTCACATTCGAGAGGACCTCAG	258	
QY	121	ACGGGCGATTGTGATGATGTGTGCTTCGGAGCTGTGATCTGAGAGGCGTTGAGATGTAC	180	
Db	259	ACAGGCGATTGTGATGATGTGTGCTTCGGAGCTGTGATCTGAGAGGCTGTGAGATGTAC	318	
QY	181	TGATTCGGCGCAAGGCTCAACAAGCAGTGTGCTTCGATCCGGGGCCCAAGGCCACACAGAC	240	
Db	319	TGTGCCCGCTGAGGCTCTCAAAAGAGGCCCGCTCTATTCGGGCCCAAGGCCACACAGTAC	378	
QY	241	ATGCCCAAGACTAGAGAGTCCAGGCCCTATTCAGACACCAAGAAAGGAAGCTCCAAAGG	300	
Db	379	ATGCCCAAGACTAGAGAGTCCCGCTTCATTCAGCAAAACAGAAACGAAGCTCCAAAGG	438	
QY	301	AGAGGAAAGGAAGTACACTTGAGAGACCAAGTGAAGGAAGTGCAGAAACAAAGACTTA	360	

Db 439 AGAAGGAAGGAAGTACATTGGAAGAACACAGTAGAGAGTGCAGAAACAGACCTA 498
 QY 361 CAGATGTAGAGAGAGCCTCCCGAGAGACAGAAATGCCGTCACCCGAAAGTCTTTG 420
 Db 489 CAGATGTAGAGAGAGCCTCCCGAGAGACAGAAATGCCGTCACCCGAAAGTCTTTG 558
 QY 421 CTGCTTGAAGCACTGCAAAACATCGAGACACCTGCGCAATATCAATTAATGATTCATA 480
 Db 559 CTGCTTGAAGCACTGCAAAACATCGAGACACCTGCGCAATATCAATTAATGATTCATA 618
 QY 481 TCATTTCAGAGATGGGCAATTCCTCCATGAAA 513
 Db 619 ACATTACAAAGATGGGCAATTCCTCCATGAAA 651
 RESULT 8
 AX147752 487 bp DNA linear PAT 08-JUN-2001
 LOCUS Sequence 11 from patent WO0136483.
 DEFINITION AX147752
 ACCESSION AX147752
 VERSION AX147752.1 GI:14346797
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 487)
 AUTHORS Goldspink, G.R. and Johnson, I.R.
 TITLE Use of the insulin-like-growth factor I isoform mgf for the
 treatment of neurological disorders
 JOURNAL Patent: WO 0136483-A 11 25-MAY-2001;
 University College London (GB)
 FEATURES
 source 1..487
 Location/Qualifiers
 CDS
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 /db_xref="GI:14346798"
 /translation="GPEITCGAELVDALQFVGSGRGFEYFNKPTVYGSIRAPQGIY
 DECCFRSCDLRLLEMYCVKCKPTKSARSIRAOHRHDMFKTQEVHLKNTSRGSAQNKI
 YRM"
 BASE COUNT 139 a 123 c 126 g 99 t
 ORIGIN
 Query Match 78.8%; Score 425; DB 6; Length 487;
 Best Local Similarity 90.4%; Pred. No. 8.8e-123;
 Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

Db 256 -----AAGGAGTACACTTGAAGAACACAACTAGAGAGATGCAGAAACAGACCTA 308
 QY 361 CAGATGTAGAGAGAGCCTCCCGAGAGACAGAAATGCCGTCACCCGAAAGTCTTTG 420
 Db 309 CAGATGTAGAGAGAGCCTCCCGAGAGACAGAAATGCCGTCACCCGAAAGTCTTTG 368
 QY 421 CTGCTTGAAGCACTGCAAAACATCGAGACACCTGCGCAATATCAATTAATGATTCATA 480
 Db 369 CTGCTTGAAGCACTGCAAAACATCGAGACACCTGCGCAATATCAATTAATGATTCATA 428
 QY 481 TCATTTCAGAGATGGGCAATTCCTCCATGAAAATCAACAGTAATGATTCATA 539
 Db 429 TCATTTCAGAGATGGGCAATTCCTCCATGAAAATCAACAGTAATGATTCATA 487

RESULT 9
 AX300789 487 bp DNA linear PAT 30-NOV-2001
 LOCUS Sequence 11 from patent WO0185781.
 DEFINITION AX300789
 ACCESSION AX300789
 VERSION AX300789.1 GI:17382070
 KEYWORDS
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1
 AUTHORS Goldspink, G.D. and Terenghi, G.B.
 TITLE Repair of nerve damage
 JOURNAL Patent: WO 0185781-A 11 15-NOV-2001;
 University College London (GB); East Grinstead Medical Research
 Trust (GB)
 FEATURES
 source 1..487
 Location/Qualifiers
 CDS
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 /db_xref="GI:17382071"
 /translation="GPEITCGAELVDALQFVGSGRGFEYFNKPTVYGSIRAPQGIY
 DECCFRSCDLRLLEMYCVKCKPTKSARSIRAOHRHDMFKTQEVHLKNTSRGSAQNKI
 YRM"
 BASE COUNT 139 a 123 c 126 g 99 t
 ORIGIN
 Query Match 78.8%; Score 425; DB 6; Length 487;
 Best Local Similarity 90.4%; Pred. No. 8.8e-123;
 Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

QY 301 AGAAGAAAGAGTACCTTGAAGACACAGTAGAGAGTGCAGAAACAGACCTA 360
 Db 256 -----AAGGAGTACACTTGAAGAACACAACTAGAGAGTGCAGAAACAGACCTA 308
 QY 361 CAGAAATGTAGAGAGGCTCTCCGAGAACAGAAATGCCAGCTACCGCAAGATCTTTG 420
 Db 309 CAGAAATGTAGAGAGGCTCTCCGAGAACAGAAATGCCAGCTACCGCAAGATCTTTG 368
 QY 421 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCAAAATCATTAATGATTCAATA 480
 Db 369 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCAAAATCATTAATGATTCAATA 428
 QY 481 TCATTTCAGAGATGGGCAATTCCTCTAATGAATACAGATTAACATTCCTCGAATTC 539
 Db 429 TCATTTCAGAGATGGGCAATTCCTCTAATGAATACAGATTAACATTCCTCGAATTC 487

RESULT 10
 RATIGFIB 1346 bp mRNA linear ROD 27-APR-1993
 LOCUS Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
 DEFINITION M15481.1 GI:204753
 ACCESSION M15481.1
 KEYWORDS growth factor; insulin-like growth factor.
 SOURCE Rat (Sprague-Dawley) adult liver, cDNA to mRNA, clone pRIGF-1-25.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 1346)
 AUTHORS Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and Lerch,D.
 TITLE Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahepatic tissues
 JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)
 MEDLINE 88288198
 PUBMED 3453891
 COMMENT Draft entry and computer-readable copy of sequence in [Mol. Endocrinol. (1987) in press] kindly provided by S.R.Lasky, 16-MAR-1987.
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 FYENKPTGSSIRAPQGTIVDECFSCDLRLNEMCVCKRPTKSRSTIRARHTD
 MPKTEVHLKNTSGSGNNTYR"
 794..859
 /note="Insulin-like growth factor signal peptide"
 mat_peptide 860..946
 /product="Insulin-like growth factor B peptide"
 mat_peptide 947..982
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 /product="Insulin-like growth factor A peptide"
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 /product="Insulin-like growth factor D peptide"
 mat_peptide 1070..1174
 /product="Insulin-like growth factor E peptide"
 BASE COUNT 348 a 344 c 344 g 310 t
 ORIGIN 1 bp upstream of EcoRI site.
 Query Match 78.3%; Score 421.8; DB 10; Length 1346;
 Best Local Similarity 90.0%; Pred. No. 1.1e-121;
 Matches 485; Conservative 0; Mismatches 2; Indels 52; Gaps 1;
 QY 1 GGACGAGAGACCTTGGGGGGGTGAGCTGTGACGCTTTCATCTGCTGTGACCA 60

Db 860 GGACGAGAGACCTTGGGGGGGTGAGCTGTGACGCTTTCATCTGCTGTGACCA 919
 QY 61 AAGGCTTTTAACTTCAACAGGCCACAGTATATGCTCAGCATTCGGAGGCGCCACAG 120
 Db 920 AAGGCTTTTAACTTCAACAGGCCACAGTATATGCTCAGCATTCGGAGGCGCCACAG 979
 QY 121 ACGGCTATTTGTAGATAGTGTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGAC 180
 Db 980 ACGGCTATTTGTAGATAGTGTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGAC 1039
 QY 181 TGTGTCCTGCAACCTTCACAAAGTCAGCTGTTTCATCCGGGCGCCACAGCTGAC 240
 Db 1040 TGTGTCCTGCAACCTTCACAAAGTCAGCTGTTTCATCCGGGCGCCACAGCTGAC 1099
 QY 241 ATGCCCAAGACTCAGAGTCCCGGCCCTATGACACACAGAAAGAGAGCTCAAAAG 300
 Db 1100 ATGCCCAAGACTCAG----- 1114
 QY 301 AGAAGAAAGAGTACACTTGAAGAACACAGTAGAGAGTGCAGAAACAGACCTA 360
 Db 1115 -----AAGGAGTACACTTGAAGAACACAGTAGAGAGTGCAGAAACAGACCTA 1167
 QY 361 CAGAAATGTAGAGAGGCTCTCCGAGAACAGAAATGCCAGCTACCGCAAGATCTTTG 420
 Db 1168 CAGAAATGTAGAGAGGCTCTCCGAGAACAGAAATGCCAGCTACCGCAAGATCTTTG 1227
 QY 421 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCCAATATGATATGAGTTCAATA 480
 Db 1228 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCCAATATGATATGAGTTCAATA 1287
 QY 481 TCATTTCAGAGATGGGCAATTCCTCTAATGAATACAGATTAACATTCCTCGAATTC 539
 Db 1288 CCATTTCAGAGATGGGCAATTCCTCTAATGAATACAGATTAACATTCCTCGAATTC 1346

RESULT 11
 RATIGFIA 1052 bp mRNA linear ROD 29-MAY-2002
 LOCUS Rattus sp. mRNA for insulin-like growth factor I precursor.
 DEFINITION complete cds.
 ACCESSION D00698
 VERSION D00698.1 GI:220780
 KEYWORDS Insulin-like growth factor I.
 SOURCE Rattus sp. liver cDNA to mRNA.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 28 to 1052)
 AUTHORS Shimatsu,A. and Rotwein,P.
 TITLE Mosaic evolution of the insulin-like growth factors. Organization, sequence, and expression of the rat insulin-like growth factor I gene.
 JOURNAL J. Biol. Chem. 262 (16), 7894-7900 (1987)
 MEDLINE 87222423
 REFERENCE 2 (bases 1 to 1052)
 AUTHORS Kato,H., Okoshi,A., Miura,Y. and Noguchi,T.
 TITLE A new cDNA clone relating to larger molecular species of rat insulin-like growth factor-I mRNA
 JOURNAL Agric. Biol. Chem. 54 (6), 1599-1601 (1990)
 MEDLINE 91103966
 COMMENT The difference in the size of IGF-I mRNA has been suggested to be primarily due to differences in the 3'-untranslated region in [1]. The cDNA clone to IGF-I mRNA reported in [2] gives direct evidence for this hypothesis.
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/protein_id="PAA00504.1"
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FYFNKPTGYSSIRAPQITVECCFRSCDLRLMYCAPLPTKSARSIRAPRHTD
MPKQKEVHLKNTSRGSGAKTYRM"
109..318
mat_peptide
/product="insulin-like growth factor mature peptide"
606
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/feature="g in [2]; deletion in [1]"
625
variation
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645
variation
/feature="a in [2]; deletion in [1]"
710..715
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731
polyA_site
/feature="polyadenylation site (putative)"
1023
polyA_site
/feature="polyadenylation site (putative)"
BASE COUNT      301 a      256 c      225 g      270 t
ORIGIN
Query Match      74.7%; Score 402.6; DB 10; Length 1052:
Best Local Similarity 88.5%; Pred. No. 1,2e-115;
Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;
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QY 1 GGACCAAGAGACCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 60
DB 109 GGACCAAGAGACCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 168
QY 61 AGGGCTTTTACTTCAACAGCCACAGTCTATGCTGCTCAGCATTCGAGGGCACCACAG 120
DB 159 AGGGCTTTTACTTCAACAGCCACAGTCTATGCTGCTCAGCATTCGAGGGCACCACAG 228
QY 121 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGATCTGAGAGAGCTGGAGATGTAC 180
DB 229 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGATCTGAGAGAGCTGGAGATGTAC 288
QY 181 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
DB 289 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 348
QY 241 ATGCCCAAGACTCAGAACTCCAGCCCTATCGACACACAAAGAAAGAGTGCACAAAG 300
DB 349 ATGCCCAAGACTCAG----- 363
QY 301 AGAAGGAAGAGAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 360
DB 364 -----AAGGAAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 416
QY 361 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATATGCCAGTACCGCAAGATCCTTG 420
DB 417 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATATGCCAGTACCGCAAGATCCTTG 476
QY 421 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATAGAGTTCATA 480
DB 477 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATAGAGTTCATA 536
QY 481 TCATTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 531
DB 537 CCATTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 587

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RESULT 12
RATGJTL      513 bp      mRNA      linear      ROD 27-APR-1993
LOCUS
DEFINITION Rat insulin-like growth factor-I mRNA, 3' end.
ACCESSION M17714
VERSION M17714.1 GI:204324
KEYWORDS insulin-like growth factor.
SOURCE Rat kidney, cDNA to mRNA.
ORGANISM Rattus norvegicus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
1 (bases 1 to 513)
AUTHORS Murphy, L.J., Bell, G.I., Duckworth, M.L. and Friesen, H.G.
TITLE Identification, characterization, and regulation of a rat
complementary deoxyribonucleic acid which encodes insulin-like
growth factor-I
JOURNAL Endocrinology 121 (2), 684-691 (1987)
MEDLINE 87246437
PUBMED 3595538
FEATURES
source
location/Qualifiers
1..513
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/db_xref="taxon:10116"
<1..513
/product="IGF-I mRNA"
<1..327
/feature="insulin-like growth factor-I precursor"
/codon_start=1
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/db_xref="GI:204325"
/translation="ATGPEPTLGCALVDLQVCGPRFYFNKPTGYSSIRAPQ
TVECCFRSCDLRLMYCAPLPTKSARSIRAPRHTDMPKQKEVHLKNTSRGSGA
KTYRM"
BASE COUNT      143 a      128 c      135 g      107 t
ORIGIN
Query Match      74.4%; Score 401; DB 10; Length 513:
Best Local Similarity 88.3%; Pred. No. 3,4e-115;
Matches 469; Conservative 0; Mismatches 10; Indels 52; Gaps 1;
1
QY 1 GGACCAAGAGACCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 60
DB 10 GGACCAAGAGACCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 69
QY 61 AGGGCTTTTACTTCAACAGCCACAGTCTATGCTGCTCAGCATTCGAGGGCACCACAG 120
DB 70 AGGGCTTTTACTTCAACAGCCACAGTCTATGCTGCTCAGCATTCGAGGGCACCACAG 129
QY 121 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGATCTGAGAGAGCTGGAGATGTAC 180
DB 130 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGATCTGAGAGAGCTGGAGATGTAC 189
QY 181 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
DB 190 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 249
QY 241 ATGCCCAAGACTCAGAACTCCAGCCCTATCGACACACAAAGAAAGAGTGCACAAAG 300
DB 250 ATGCCCAAGACTCAG----- 264
QY 301 AGAAGGAAGAGAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 360
DB 265 -----AAGGAAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 317
QY 361 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATATGCCAGTACCGCAAGATCCTTG 420
DB 318 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATATGCCAGTACCGCAAGATCCTTG 377
QY 421 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATAGAGTTCATA 480
DB 376 CTGCTTGAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATAGAGTTCATA 437
QY 481 TCATTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 531
DB 438 CCATTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 488

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RESULT 13
RATGIFR
LOCUS      521 bp      mRNA      linear      ROD 13-JUL-1995
DEFINITION Rat mRNA for insulin-like growth factor I (IGF-I).
ACCESSION X06043.M17714
VERSION    X06043.1 GI:56434
KEYWORDS   Insulin-like growth factor I.
SOURCE     Rattus norvegicus.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 521)
AUTHORS   Murphy,L.J., Bell,G.I., Duckworth,M.L. and Friesen,H.G.
TITLE      Identification, characterization, and regulation of a rat
            complementary deoxyribonucleic acid which encodes insulin-like
            growth factor-I
JOURNAL    Endocrinology 121 (2), 684-691 (1987)
MEDLINE    87246437
PUBMED     3585538
COMMENT    Data kindly reviewed (11-FEB-88) by Murphy L. J.
FEATURES   Source
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            /db_xref="taxon:10116"
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            /db_xref="SWISS-PROT:P08025"
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            misc_feature      97..132
                               /note="C domain (AA 30-41)"
            misc_feature      133..195
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            misc_feature      196..219
                               /note="D domain (AA 63-70)"
            BASE COUNT      151 a      128 c      135 g      107 t
            ORIGIN
Query Match      74.4%; Score 401; DB 10; Length 521;
Best Local Similarity 88.3%; Pred. No. 3.4e-115;
Matches 469; Conservative 0; Mismatches 10; Indels 52; Gaps 1;

QY      1 GGACCAAGAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCAGTCTGTGTGACCA 60
        |||||||
DB      10 GGACCAAGAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCAGTCTGTGTGACCA 69
QY      61 AGGGGCTTTACTTCAACAAGCCCAAGTCTATGCTCAGATTCGAGGGGACACAG 120
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DB      70 AGGGGCTTTACTTCAACAAGCCCAAGGCTATGCTCAGATTCGAGGGGACACAG 129
QY      121 ACGGGCATTTGTGATGATGTTGTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
        |||||||
DB      130 ACGGGCATTTGTGATGATGTTGTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 189
QY      181 TGTGTCGGCTGACAGCTTACCAAGTCAAGTCTGCTTCATCCGGGCCACAGCACTGAC 240
        |||||||
DB      190 TGTGTCGGCTGACAGCTTACCAAGTCAAGTCTGCTTCATCCGGGCCACAGCACTGAC 249
QY      241 ATGCCCAAGACTCGAAGTCCCAAGCCCTATTCACACACAGAAAGAGCTGCAAG 300
        |||||||
DB      250 ATGCCCAAGACTCGAAGTCCCAAGCCCTATTCACACACAGAAAGAGCTGCAAG 300
QY      301 AGAAGAAGAGAGTACCTTGAAGACACAGTAGAGAGAGTGCAGAAAGACCTTA 360
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DB      265 -----AAGGAAGTACCTTGAAGACACAGTAGAGAGAGTGCAGAAAGACCTTA 317

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QY      361 CAGATGTAGAGAGAGGCTCCCGAGAGACAGAAATGCCACGTCACCGGACAGATCTTGG 420
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DB      318 CAGATGTAGAGAGAGGCTCCCGAGAGAGAGAAATGCCACGTCACCGGACAGATCTTGG 377
QY      421 CTGCTTGAGGACACCTGCAAAACATGGAACACCTGCGCAATATCAATTAATGAGTTCAATA 480
        |||||||
DB      378 CTGCTTGAGGACACCTGCAAAACATGGAACACCTGCGCAATATCAATTAATGAGTTCAATA 437
QY      481 TCATTTCAGAGATGGGCAATTCCTCCATCAATGAATTAACACAGTAACATCTCC 531
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DB      438 CCATTTCAGAGATGGGCAATTCCTCCATCAATGAATTAACACAGTAACATCTCC 488

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RESULT 14
RATGIFR
LOCUS      826 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION M17335.1
VERSION    M17335.1 GI:204751
KEYWORDS   Insulin-like growth factor I.
SOURCE     Rat (Sprague Dawley) testis, cDNA to mRNA, clone p2.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 826)
AUTHORS   Casella,S.J., Smith,E.P., van Wyk,J.J., Joseph,D.R., Hynes,M.A.,
            Hoyt,E.C. and Lund,P.K.
TITLE      Isolation of rat testis cDNAs encoding an insulin-like growth
            factor I precursor
JOURNAL    DNA 6 (4), 325-330 (1987)
MEDLINE    88003970
PUBMED     3652906
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            /db_xref="taxon:10116"
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            BASE COUNT      223 a      214 c      181 g      208 t
            ORIGIN
Query Match      71.8%; Score 387; DB 10; Length 826;
Best Local Similarity 88.0%; Pred. No. 9.7e-111;
Matches 455; Conservative 0; Mismatches 10; Indels 52; Gaps 1;

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	539	100.0	539	24	AAS16876
3	425	78.8	487	22	AAD06404
4	425	78.8	487	24	AAS16883
5	402.6	74.7	1052	20	AAX27498
6	356.8	66.2	523	22	AAD06400
7	356.8	66.2	523	24	AAS16879
8	356.8	66.2	553	18	AAT84893
9	325.2	60.3	517	22	AAD06398

10	325.2	60.3	517	24	AAS16877
11	274.2	50.9	818	8	AAN70436
12	274.2	50.9	7260	24	ABK84583
13	274.2	50.9	7260	24	ABN97244
14	274.2	50.9	7260	24	ABK64812
15	274.2	50.9	7260	24	ABK35504
16	274.2	50.9	7260	24	ABK35561
17	272.6	50.6	777	18	AAT84894
18	271	50.3	622	7	AAN60490
19	262	48.6	471	22	AAD06405
20	262	48.6	471	24	AAS16884
21	231	42.9	1136	8	AAN70435
22	230.2	42.7	978	14	AAN047804
23	224	41.6	612	22	AAS16895
24	222	41.2	3599	19	AAV50428
25	222	41.2	3599	19	AAV40796
26	222	41.2	3600	19	AAV50427
27	222	41.2	3600	19	AAV40795
28	222	41.2	5707	20	AAV88055
29	222	41.2	6345	20	AAV88054
30	206.8	38.4	317	24	AAS16882
31	206.8	38.4	318	22	AAD06403
32	206.8	38.4	462	19	AAV50426
33	206.8	38.4	462	19	AAV40794
34	206.8	38.4	462	24	ABL91699
35	168.4	31.2	210	24	ABA03146
36	168.8	30.9	237	12	ABA013566
37	168.8	30.9	238	12	AAQ13566
38	168.8	30.9	2862	19	AAV26283
39	165.2	30.6	207	22	AAH22139
40	165.2	30.6	462	19	AAV50425
41	165.2	30.6	462	19	AAV40793
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ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description
1	539	100.0	539	22	AAD06399
2	539	100.0	539	24	AAS16876
3	425	78.8	487	22	AAD06404
4	425	78.8	487	24	AAS16883
5	402.6	74.7	1052	20	AAX27498
6	356.8	66.2	523	22	AAD06400
7	356.8	66.2	523	24	AAS16879
8	356.8	66.2	553	18	AAT84893
9	325.2	60.3	517	22	AAD06398

Human mechano-growth factor (MGF) cDNA.
Rat IGF-I isoform mechano-growth factor (MGF) cDNA.
Rat IGF-I isoform; Insulin-like Growth Factor-I; MGF;
mechano-growth factor; neurological disorder; neurodegenerative disorder;
amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
polymyositis; post-polio syndrome; toxins; myoneurone disorder;
nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
sex-linked muscular dystrophy; peripheral neuropathy;
Alzheimer's disease; Parkinson's disease; ss.
Rattus sp.
Key CDS
Location/Qualifiers
1..336
/*tag= a
/*product= "Mechano-growth factor (MGF)"
/note= "This region comprises exons 3-6. The CDS does not include start codon"
/partial

PF 15-NOV-2000; 2000MO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldslink G, Johnson I;
 XX
 DR WPI: 2001-355620/37.
 DR P-PSDB: AA02448.
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder.
 XX
 PS Claim 4: Page 51-52; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneuron loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
 CC injury that affects motoneurons, motoneuron loss associated with aging,
 CC peripheral or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (EC) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX
 XX
 SQ Sequence 539 BP: 161 A; 136 C; 139 G; 103 T; 0 other;
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 Best Local Similarity 100.0%; Pred. No. 2,3e-142;
 Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 CTTGTTGAGCAACCTCGCAAAACATCGGAGACCTCGCCCAATATCAATGATTCATAA 480
 OY 481 TCATTTCAGAGATGGGCACTTTCCCTCAATGAATACAGTAACATTTCCGGAAATTC 539
 DB 481 TCATTTCAGAGATGGGCACTTTCCCTCAATGAATACAGTAACATTTCCGGAAATTC 539
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 ID AAS16878
 ID AAS16878 standard; cDNA, 539 BP.
 AC AAS16878;
 XX
 XX 25-FEB-2002 (first entry)
 DT
 XX
 DE Rat mechano-growth factor (MGF) cDNA.
 XX
 KM Rat: mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KM neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KM muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KM nerve avulsion.
 XX
 OS Rattus sp.
 XX
 FH Key
 FH CDS
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 FT /product= "Rat MGF"
 FT /partial
 FT /note= "No start codon"
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 FT /number= exon 3
 FT 76..258
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 PN MO200185781-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001MO-GB02054.
 PR 10-MAY-2000; 2000GB-0011278.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX
 PI Goldslink G, Terenghi I;
 XX
 DR WPI: 2002-055685/07.
 DR P-PSDB: AAU10560.
 XX
 PT Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to
 PT treat nerve damage
 XX
 PS Disclosure: Fig 6; 65pp; English.
 XX
 CC The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth

KW diabetic; ss.
 XX
 OS Rattus sp.
 XX
 PN W0910013-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 25-AUG-1998; 98WO-US17428.
 XX
 PR 25-AUG-1997; 97US-0057201.
 XX
 PA (MASC-) MASSACHUSETTS GEN HOSPITAL.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Rosenthal NA, Sweeney HL;
 XX
 DR WPI; 1999-190469/16.
 XX
 PT Use of modified insulin-like growth factor I - in gene therapy for
 PT increasing vertebrate muscle strength and mass
 PS
 PS Example 1; Fig 4; 46pp; English.
 CC This sequence represents the liver isoform of the rat insulin-like
 CC growth factor I (IGF-I) from rats. IGF-I or a modified or biologically
 CC active portion can be used for increasing vertebrate muscle mass by
 CC intramuscular administration, for e.g. (i) preserving or enhancing
 CC muscle strength in aging humans; (ii) healing injured muscle more
 CC efficiently/rapidly; (iii) controlling muscle mass during disease and/or
 CC prolonged stays in reduced gravity; (iv) cosmetic body sculpting; and
 CC (v) promoting glucose clearance from diabetic muscle tissue.
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 XX Sequence 1052 BP; 301 A; 256 C; 225 G; 270 T; 0 other;
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 Query Match 74.7%; Score 402.6; DB 20; Length 1052;
 Best Local Similarity 88.5%; Pred. NO. 9.8e-104;
 Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;
 QY 1 GGACCGAGACCCCTTGGCGGGCTGAGCTGTGAGACGCTTCAGTGTGTGAGACCA 60
 DB 109 GGACCGAGACCCCTTGGCGGGCTGAGCTGTGAGACGCTTCAGTGTGTGAGACCA 168
 QY 61 AGGGCTTTACTTCAACAGCCACAGCTATGCTCCAGCATTCGGAGGCGACACAG 120
 DB 169 AGGGCTTTACTTCAACAGCCACAGCTATGCTCCAGCATTCGGAGGCGACACAG 228
 QY 121 ACGGGCATTTGATGATGATGATGCTTCCGAGCTGTATGAGAGAGCGCTGAGATGTAC 180
 DB 229 ACGGGCATTTGATGATGATGATGCTTCCGAGCTGTATGAGAGAGCGCTGAGATGTAC 288
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 QY 421 CTGCTTGAGCAACCTGCAAAAACATCGGAACACTGCCCAATATCAATATGAGTTCAATA 480
 DB 477 CTGCTTGAGCAACCTGCAAAAACATCGGAACACTGCCCAATATCAATATGAGTTCAATA 536
 QY 481 TCATTTCAGAGATGGGCAATTCCTCAATGAATACACAAAGTAACATTC 531
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DB 537 CCATTTCAGAGATGGGCAATTCCTCAATGAATACAAAGTAACATTC 587
 RESULT 6
 AAD06400
 ID AAD06400 standard; CDNA; 523 BP.
 XX
 AC AAD06400;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Rabbit IGF-I isoform mechano-growth factor (MGF) CDNA.
 XX
 KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
 KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 FH Key Location/Qualifiers
 FH 1..336
 FT CDS /tag= a
 FT /product= "Mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial
 XX
 PN W0200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
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 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldsprint G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 XX
 PS P-PSDB; AAE02449.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder.
 XX
 PS Claim 4; Page 53-54; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (EC) domain, hence also referred as
 CC IGF-1-EC. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 66.2%; Score 356.8; DB 22; Length 523;
Best Local Similarity 82.3%; Pred. No. 6,7e-91;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

OY 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCAAGTGGTGGGACCA 60
DB 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCAAGTGGTGGGACCA 60
OY 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATAGGCTCCAGCATTCGGAGGACCAAG 120
DB 61 AGGGGCTTTTATTTCAACAAAGCCACAGTATAGGCTCCAGCATTCGGAGGACCAAG 120
OY 121 ACAGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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OY 481 TCATTTCAAGATGGGATTTCCCTCAATGAATTAACAAAGTAACATTC 530
DB 481 TCATTTCAAGATGGGATTTCCCTCAATGAATTAACAAAGTAACATTC 530
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RESULT 7
AAS16879
ID AAS16879 standard; cDNA; 523 BP.

XX AAS16879;
AC AAS16879;
XX 25-FEB-2002 (first entry)

DE Rabbit mechano-growth factor (MGF) cDNA.
XX Rabbit mechano-growth factor (MGF) cDNA.

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
XX nerve avulsion.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

FT CDS 1..336
FT /tag= a
FT /product= "Rabbit MGF"
FT /partial
FT /note= "No start codon"
FT 1..76
FT /tag= b
FT /number= 3
FT exon 77..259
FT /tag= c
FT /number= 4
FT exon 260..309

FT /tag= d
FT /number= 5
FT exon 311..333
FT /tag= e
FT /number= 6

MO200185781-A2.

15-NOV-2001.

10-MAY-2001; 2001WO-GB02054.

10-MAY-2000; 2000GB-0011278.

(UNLO) UNIV COLLEGE LONDON.

(EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

Goldsplink G, Terenghi G;

WPI: 2002-055585/07.

P-PSDB; AAI10561.

Use of insulin-like growth factor I (IGF-I) isoform known as mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has ability to reduce motoneuron loss in response to nerve avulsion, to treat nerve damage

Disclosure: Fig 7; 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture of a medicament for treating nerve damage in the peripheral nervous system, or for treating nerve damage by localising MGF at the site of damage. The nerve damage may include severing of a nerve. The treatment may be combined with another treatment (such as a polypeptide growth factor other than MGF) that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates, whereby the treatment of the muscle with MGF or a polynucleotide encoding MGF prevents or diminishes degeneration. The method is useful for CC treating neurological disorders, preferably motoneuron disorders. These CC methods can reduce motoneuron loss by 20% or greater in response to nerve CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 66.2%; Score 356.8; DB 24; Length 523;
Best Local Similarity 82.3%; Pred. No. 6,7e-91;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

OY 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCAAGTGGTGGGACCA 60
DB 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCAAGTGGTGGGACCA 60
OY 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATAGGCTCCAGCATTCGGAGGACCAAG 120
DB 61 AGGGGCTTTTATTTCAACAAAGCCACAGTATAGGCTCCAGCATTCGGAGGACCAAG 120
OY 121 ACAGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 ACAGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
OY 181 TGTGTCGCTGCAAGCTTACAAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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OY 301 AGAAGGAAGAAAGTACACTTGAAGAACACACAGTAGAGAGAGTGCAGAAACAGACTA 360
DB 301 AGAAGGAAGAAAGTACACTTGAAGAACACACAGTAGAGAGAGTGCAGAAACAGACTA 360

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QY 361 CAGATGTAGAGAGACCTCCCGAGACAGAAATGCCAGCTCACCGCAGATCCTTTG 420
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Db 361 CAGATGTAGAGAGACCTCTCTAGAGATGACAGACAGCCACCGACGACCTTTG 420
QY 421 CTGCTTGAGCAACCTGCAAAACATCGAGACACCTGCCAATATCAATATGAGTTCAATA 480
    ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||
Db 421 CTCTGCACAGTTACCTGTAAACATGTGAATACCGGCCA-----AAAAATAAGTTGATC 474
QY 481 TCATTTAGAGATGGGATTTCCCTCAATGAATACAGATAACATTC 530
    ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 ACATTTCAGAGAT-GGCATTTCCCGCAATGAATACAGATAACATTC 523

RESULT 8
AAT84893
ID AAT84893 standard; cDNA; 553 BP.
XX
AC AAT84893;
XX
DT 14-APR-1998 (first entry)
XX
DE Rabbit insulin like growth factor 1 encoding cDNA.
XX
KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW heart; neuromuscular disease; primer; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..366
FT /tag= a
FT /product= "IGF-1"
XX
XX MO9733997-A1.
XX
XX 18-SEP-1997.
XX
XX PF 11-MAR-1997; 97WO-GB00658.
XX
XX PR 11-MAR-1996; 96GB-0005124.
XX
XX (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
XX Goldslink G;
XX
XX WPI: 1997-470877/43.
XX
XX P-PSDB; AAM23301.
XX
XX
XX Use of insulin like growth factor I characterised by presence of Ec
XX peptide - to treat humans or animals, particularly muscle disorders,
XX heart conditions or neuromuscular diseases
XX
XX Disclosure; Fig 3; 33pp; English.
XX
XX A use of insulin like growth factor I (IGF-1) has been developed, and
XX is characterised by the presence of the Ec peptide, or a functional
XX equivalent, in the treatment or therapy of a human or animal. The IGF-1
XX polypeptide can be used to treat muscular disorders, e.g. Duchenne or
XX Becker muscular dystrophy, autosomal dystrophies and related progressive
XX skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
XX spinal cord injury induced muscle atrophy and neuromuscular diseases,
XX and cardiac disorders, e.g. diseases where promotion of cardiac muscle
XX protein synthesis is a beneficial treatment, cardiomyopathies and acute
XX heart failure or insulin, specifically myocarditis or myocardial
XX infarction. It can also be used to promote bone fracture healing and
XX maintenance of bone in old age. The present sequence encodes rabbit
XX IGF-1 used in the present specification.
XX
XX Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;
XX
Query Match 66.2%; Score 356.8; DB 18; Length 553;
Best Local Similarity 82.3%; Pred No. 6,8e-91;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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QY 1 GCACAGAGACCTTTGGCGGCTGAGCTGTGAGACGCTCTTCAGTTGTGTGAGACA 60
    ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||
Db 31 GCACCGGAGACCTCTCGCGTGTGAGCTGTGAGTCTTCAGTTGTGTGAGAC 90
QY 61 AGGGCTTTTACTTAACAAGCCGACACTGATATGCTCCACATTCCGAGGGCACACAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 AGGGCTTTTATTTAACAAGCCGACAGATACGCTCCACAGTCGAGGGCACCTCAG 150
QY 121 AGGGCATTTGTGATGATGTGTCTTCGAGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 ACAGCATCTGTGATGATGTGTCTTCGAGAGCTGTGATCTGAGAGGCTGAGATGTAC 210
QY 181 TGTGTCCCTGTGAACCTTCACAAAGTCACCTGTTCCATCCGCGCCACGACACTGAC 240
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 TGTGCACCCCTCAAGCCGCAAGGACGCGCTCCGTCGCTGCGCCACGCGCACCGAC 270
QY 241 ATGCCCAAGACTCAAGAAATCCGAGCCCTATCGACACACAGAAAGAAAGCAAGCTCAAAAG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 ATGCCCAAGACTCAAGAAATATCAGCTTCATCTACAAAGAAATGATGATCTCAGAGG 330
QY 301 AGAAGAAAGAGAGTACACTTGAAGACACAAAGTAGAGAAAGTCCAGAGAAAGACCTA 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 AGAAGAAAGAGAGTACACTTGAAGACACAAAGTAGAGAGGAGTCCAGAGAAAGACACTA 390
QY 361 CAGATGTAGAGAGACCTCCCGAGAGACAGAAATGCCAGTCCAGCAGATCCTTTG 420
    ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||
Db 391 CAGATGTAGAGAGACCTCTTGAGAGTGAAGAGGACAGCCACCGACGACCTTTG 450
QY 421 CTGCTTGAGCAACCTGCAAAACATCGAACACCTGCCAATAATCAATATGAGTTCAATA 480
    ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||
Db 451 CTCTGCACAGTTACCTGTAAACATGTGAATACCGGCCA-----AAAAATAAGTTGATC 504
QY 481 TCATTTAGAGATGGGATTTCCCTCAATGAATACAGATAACATTC 530
    ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 ACATTTCAGAGAT-GGCATTTCCCGCAATGAATACAGATAACATTC 553

RESULT 9
AAD06398
ID AAD06398 standard; cDNA; 517 BP.
XX
XX AAD06398;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
XX Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
XX mechano-growth factor; neurological disorder; neurodegenerative disorder;
XX amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
XX poliomyelitis; post-polio syndrome; toxin; motoneuron disorder;
XX nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
XX sex-linked muscular dystrophy; peripheral neuropathy;
XX Alzheimer's disease; Parkinson's disease; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..333
XX /tag= a
XX /product= "Mechano-growth factor (MGF)"
XX /note= "This region comprises exons 3-6. The CDS does
XX not include start codon"
XX
XX W0200136483-A1.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-GB04354.
XX
XX 15-NOV-1999; 99GB-0026968.

```

XX (UNLO) UNIV COLLEGE LONDON.
PA Goldslink G, Johnson I;
XX WPI: 2001-355620/37.
XX P-PSDB: AAE02447.

DR Use of mechano-growth factor, an isoform of insulin-like growth
PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
PT medicament for the treatment of neurological disorder .
XX
XX

PS Claim 4: Page 49-50; 66pp; English.

XX The present invention relates to use of mechano-growth factor (MGF),
CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneuron loss by 20% or greater in response to nerve
CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurons and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy, progressive
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
CC injury that affects motoneurons, motoneuron loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (EC) domain, hence also referred as
CC IGF-I-EC. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX

SQ Sequence 517 BP: 150 A; 130 C; 139 G; 98 T; 0 other:

Query Match 60.3%; Score 325.2; DB 22; Length 517;
Best Local Similarity 81.2%; Pred. No. 5.6e-82;
Matches 429; Conservative 0; Mismatches 88; Indels 11; gaps 4;

QY 1 GGACCCAGAGACCCCTTTCGGGGCTGAGCTGGAGACCTCTTCACTGCTGTGGACCA 60
DB 1 GGACCCAGAGACCCCTTTCGGGGCTGAGCTGGAGACCTCTTCACTGCTGTGGACCA 60
QY 61 AGGGGCTTTACTTCAACAAGCCCAAGCTATGCTCCAGCAATTCGAGGCGCACCA 120
DB 61 AGGGGCTTTACTTCAACAAGCCCAAGCTATGCTCCAGCAATTCGAGGCGCACCA 120
QY 121 ACGGCGATTTGATGATGATGCTGCTCCGAGGCTGATGAGAGGCTGGAGATGAC 180
DB 121 ACGGCGATTTGATGATGATGCTGCTCCGAGGCTGATGAGAGGCTGGAGATGAC 180
QY 181 TGTGTCCGCTGACCTCAACAAGCTGCTGTCCATCGGAGCCGCGCCACTGAC 240
DB 181 TGTGTCCGCTGACCTCAACAAGCTGCTGTCCATCGGAGCCGCGCCACTGAC 240
QY 241 ATGCCCAAGACTAGAGTCCGAGCCCTATGACACACAAGAAAGAGAGCTGCAAG 300
DB 241 ATGCCCAAGACTAGAGTCCGAGCCCTATGACACACAAGAAAGAGAGCTGCAAG 300
QY 301 AGAAGGAAGGAAGTCACTTGAAGAACAACAAGTAGAGAGTGCAGAAACAAGACTA 360
DB 301 AGAAGGAAGGAAGTCACTTGAAGAACAACAAGTAGAGAGTGCAGAAACAAGACTA 360
QY 361 CAGAATGAGAGAGAGCTCCGAGAGACAGAAATGCCAGCTACCCGCAAGTCTTTG 420
DB 361 CAGAATGAGAGAGCTCCGAGAGACAGAAATGCCAGCTACCCGCAAGTCTTTG 420
QY 421 CTCTGACAGTACCTGTAACATTTGAAATACCGGCCA-----AAATAATAGTTTGA 480
DB 421 CTCTGACAGTACCTGTAACATTTGAAATACCGGCCA-----AAATAATAGTTTGA 480
QY 470

OY 481 TCATTTCAGAGAGGAGCTTCCCTCATGAAATACCAAGTAACAT 528
DB 471 ACATTTCAGAGAT-GGCAATTCCTCCCAATGAATAACAAAGTAACAT 517

RESULT 10

AA16877
ID AA16877 standard; cDNA; 517 BP.
XX
XX AA16877;
AC
XX
DT 25-FEB-2002 (first entry)
XX

DE Human mechano-growth factor (MGF) cDNA.

XX Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
XX nerve avulsion.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..333

FT /tag= a

FT /product= "Human MGF"

FT /partial

FT /note= "No start codon"

FT /tag= b

FT /number= 3

FT /tag= c

FT /number= 4

FT /tag= d

FT /number= 5

FT /tag= e

FT /number= 6

PN MO200185781-A2.

PD 15-NOV-2001.

XX 10-MAY-2001; 2001MO-GB02054.

PR 10-MAY-2000; 2000GB-0011278.

XX (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

PI Goldslink G, Terenghi G;

DR WPI: 2002-055585/07.

XX P-PSDB: AA105559.

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage .

PS Claim 11; Fig 5; 65pp; English.

XX The invention relates to the use of an insulin-like growth factor I

CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motor neuron disorders. These
 CC methods can reduce locomotion loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the human MGF.

XX Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 60.3%; Score 325.2; DB 24; Length 517;
 Best Local Similarity 81.2%; Pred. No. 5,6e-82;
 Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

1 GGACGAGAGACCCCTTTCGCGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGCA 60
 1 GGACCGGAGAGCGCTGCGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGCA 60
 61 AGGGGCTTTACTTCAACAAGCCGACAGCTATGCTCCAGCATTCGAGGGGACCCACAG 120
 61 AGGGGCTTTACTTCAACAAGCCGACAGGGATGCTCCAGCATTCGAGGGGACCCCTCAG 120
 121 AGGGGCTTTACTTCAACAAGCCGACAGGGATGCTCCAGCATTCGAGGGGAGGTGATG 180
 121 ACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGCGCCAGCCCACTGAC 240
 181 TGGGCAACCCCTCAAGCTGCAAGTCAAGCTGCTCCATCCGCGCCAGCCCACTGAC 240
 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGAAG 300
 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGAAG 300
 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGAAG 297
 301 AGAAGAAAGAGAGTACACTTGAAGACAAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 360
 298 AGAAGAAAGAGAGTACACTTGAAGACAAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 357
 361 CAGATGTAGAGAGAGTCCCGAGAGACAGAAATGCCAGTCAACCCAGATCTTTG 420
 358 CAGATGTAGAGAGAGTCCCGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGT 416
 421 CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 480
 417 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCA-----AAAATATAGTTGATC 470
 481 TCATTTGAGAGATGAGGCAATTCCTCATGGAATACAAAGTGAATCAAT 528
 471 ACATTTCAAGAT-GGCATTTTCCCAATGAATACAGAGTGAATCAAT 517

RESULT 11
 AAN70436
 ID AAN70436 standard; cDNA; 818 BP.

AC AAN70436;
 DT 05-APR-1991 (first entry)

XX Sequence encoding insulin-like growth factor 1A (IGF-1A).

XX Growth promoter; lactation enhancer; cell proliferation; ss.

XX Homo sapiens.

XX EP229750-A.

XX 22-JUL-1987.

XX 06-JAN-1987; 87EP-0870001.

XX 20-NOV-1986; 86US-0928671.

XX 07-JAN-1986; 86US-0816662.

XX (UNIT) UNIV OF WASHINGTON.

PI Krivi GG, Rotwein PS;
 XX WPI; 1987-200203/29.

PT New pre-insulin-like growth factor-1 protein - obt'd. by
 PT recombinant DNA procedures for use as growth promoters for
 PT enhancing lactation, for stimulating cell proliferation etc.

XX Example; Fig 5; 59pp; English.

CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
 CC amino acids 10 to 23 of mature human IGF-1 was synthesized (AAN70437).
 CC The radiolabeled 42 mer was then employed to screen for IGF-1
 CC containing DNA sequences in a human liver cDNA library. Insulin-
 CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
 CC library by using lambda phage 11 (AAN70435, AAN70436). The human IGF-1
 CC genomic gene was isolated and mapped. It encodes at least two
 CC preproinsulin-like growth factor-1 proteins. An essentially pure
 CC preproinsulin-like growth factor-1 protein comprising the sequence
 CC of amino acids shown in figure six is claimed (AAN70277).

XX Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 50.9%; Score 274.2; DB 8; Length 818;
 Best Local Similarity 76.0%; Pred. No. 1.7e-67;
 Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

1 GGACGAGAGACCCCTTTCGCGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGCA 60
 1 GGACCGGAGAGCGCTGCGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGCA 60
 203 GGACCGGAGAGCGCTGCGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGCA 262
 61 AGGGGCTTTACTTCAACAAGCCGACAGCTATGCTCCAGCATTCGAGGGGACCCACAG 120
 263 AGGGGCTTTACTTCAACAAGCCGACAGGGATGCTCCAGCATTCGAGGGGACCCCTCAG 322
 121 AGGGGCTTTACTTCAACAAGCCGACAGGGATGCTCCAGCATTCGAGGGGAGGTGATG 180
 121 ACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 323 ACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382
 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGCGCCAGCCCACTGAC 240
 383 TGGGCAACCCCTCAAGCTGCAAGTCAAGCTGCTCCATCCGCGCCAGCCCACTGAC 442
 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGAAG 300
 443 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGAAG 457
 301 AGAAGAAAGAGAGTACACTTGAAGACAAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 360
 458 -----AAGAAAGTACACTTGAAGACAAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 510
 361 CAGATGTAGAGAGAGTCCCGAGAGACAGAAATGCCAGTCAACCCAGATCTTTG 420
 511 CAGATGTAGAGAGAGTCCCGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 570
 421 -CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 478
 571 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCA-----AAAATATAGTTGATC 624
 479 TATCATTTGAGAGATGAGGCAATTCCTCATGGAATACAAAGTGAATCAATCAATTC 531
 625 TATCATTTGAGAGATGAGGCAATTCCTCATGGAATACAAAGTGAATCAATCAATTC 677

RESULT 12
 ABR84583
 ID ABR84583 standard; cDNA; 7260 BP.

AC ABR84583;

DT 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #1154.

Human; ss: granulocytic cell; DNA chip; bacterial infection;
 KM viral infection; parasitic infection; protozoal infection;
 KM fungal infection; sterile inflammatory disease; psoriasis;
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KM adult respiratory distress syndrome; inflammatory bowel disease;
 KM Crohn's disease; ulcerative colitis; periodontal disease;
 KM granulocyte activation; chronic inflammation; allergy.
 XX
 CS Homo sapiens.
 XX
 PN W0200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001MO-US30821.
 XX
 FR 03-OCT-2000; 2000US-237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaoka S., Vockley J;
 DR WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX
 PS Claim 1; SEQ ID No 1154; 114pp: English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC or allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection, and
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct-sequences.
 XX
 Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

[illegible]

PT Liver tissue sample -
XX
XX Claim 1, SEQ ID NO 3742; 298bp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytosolic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
Query Match 50.9%; Score 274.2; DB 24; Length 7260;
Best Local Similarity 76.0%; Pred. No. 3,6e-67;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;
QY 1 GGACCGAGAGACCCCTTGGGGGGCTGAGCTGAGAGCTTCTGAGTTCGTTGTTGAGCA 60
DB 311 GGACCGAGAGACCTCTGCGGGGCTGAGCTGAGAGCTTCTGAGTTCGTTGTTGAGCA 370
QY 61 AGGGGCTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTTGGAGGGCCACACAG 120
DB 371 AGGGGCTTTATTTTAAACAAGCCCAAGGTTATGCTCCAGCATTTGGAGGGCCCTCAG 430
QY 121 ACGGGCATTTGGATAGATGTTGCTTCCGGAGCTTGATCTGGAGAGCTGAGAGTAC 180
DB 431 ACGGGCATTTGGATAGATGTTGCTTCCGGAGCTTGATCTGGAGAGCTGAGAGTAC 490
QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCACTGCTTCCATCCGGGGCCAGCGCCACTGTAC 240
DB 491 TGGGCAACCTCTCAAGCTGCGCAAGTCAAGTCTGCTGTGCTGCGTCCAGCGCCACACGAG 550
QY 241 ATGCCCAAGCTCAGAGTCCCAAGCCCTTATGCACACACAAGAAAGAGCTGCAAG 300
DB 551 ATGCCCAAGCTCAGAGTCCCAAGCCCTTATGCACACACAAGAAAGAGCTGCAAG 565
QY 301 AGAAGCAAGAGTACACTTGAAGAACAAGTAGAGAGTGCAGAAACAAGACTA 360
DB 566 -----AAGGAGTACATTGTAAGAAAGCAAGTAAAGGAGTGCAGAAACAAGACTA 618
QY 361 CAGAAATGTAGAGAGCTCCGAGGAACAAGAAATGCCAGTCCAGCAAGATCCTTTG 420
DB 619 CAGAAATGTAGAGAGCTCCGAGGAACAAGAGTGAAGAGTACATGCCAGGAGATCCTTTG 678
QY 421 --CTGGCTTGAGCAACCTGCAAAACATCGGAACACTGCCCAATATCAATAGTTCAA 478
DB 679 CTCTGACGAGTTRACCTTGAACCTTTGAGACACCTTACA-----AAATAATAGTTTGA 732
QY 479 TATCATTTAGAGATGGGCAATTTCCCTCAATGAATACAACTAATCAATTC 531
DB 733 TACATATTAAAGATGGGCGTTTCCCGCAATGAATACAACTAATCAATTC 785
RESULT 14
ABK64812
ID ABK64812 standard; DNA; 7260 BP.
AC ABK64812;
XX
XX 18-JUN-2002 (first entry)
DT
DE Human benign prostatic hyperplasia gene #707.
XX

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
XX Homo sapiens.
OS
XX MO200212440-A2.
PN
XX 14-FEB-2002.
PD
XX
PF 07-AUG-2001; 2001WO-US24708.
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
XX (GENE-) GENE LOGIC INC.
PA (NIBS) JAPAN TOBACCO INC.
XX
XX Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
XX cells
XX
PS Disclosure; Page 391-393; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
Query Match 50.9%; Score 274.2; DB 24; Length 7260;
Best Local Similarity 76.0%; Pred. No. 3,6e-67;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;
QY 1 GGACCGAGAGACCCCTTGGGGGGCTGAGCTGAGAGCTTCTGAGTTCGTTGTTGAGCA 60
DB 311 GGACCGAGAGACCTCTGCGGGGCTGAGCTGAGAGCTTCTGAGTTCGTTGTTGAGCA 370
QY 61 AGGGGCTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTTGGAGGGCCACACAG 120
DB 371 AGGGGCTTTATTTTAAACAAGCCCAAGGTTATGCTCCAGCATTTGGAGGGCCCTCAG 430
QY 121 ACGGGCATTTGGATAGATGTTGCTTCCGGAGCTTGATCTGGAGAGCTGAGAGTAC 180
DB 431 ACGGGCATTTGGATAGATGTTGCTTCCGGAGCTTGATCTGGAGAGCTGAGAGTAC 490
QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCACTGCTTCCATCCGGGGCCAGCGCCACTGTAC 240
DB 491 TGGGCAACCTCTCAAGCTGCGCAAGTCAAGTCTGCTGTGCTGCGTCCAGCGCCACACGAG 550
QY 241 ATGCCCAAGCTCAGAGTCCCAAGCCCTTATGCACACACAAGAAAGAGCTGCAAG 300

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 43.6935 seconds
(without alignments)
3783.145 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggaccagagacccttgcgg.....agtaacattcccggaattc 539

Scoring table: IDENTITY_NIC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.8	66.2	553	4	US-09-142-583A-3
2	356.8	66.2	553	4	US-09-142-583A-5
3	272.6	50.6	777	4	US-09-142-583A-10
4	271	50.3	632	6	5405942-2
5	222	41.2	5707	2	US-08-472-809B-8
6	222	41.2	6345	2	US-08-472-809B-7
7	205.2	38.1	357	6	5405942-9
8	203.6	37.8	357	6	5405942-13
9	166.8	30.9	210	6	5405942-7
10	166.8	30.9	210	6	5405942-11
11	166.8	30.9	2862	4	US-09-255-829-13
12	165.2	30.6	210	6	5405942-15
13	161.2	29.9	240	1	US-08-308-196A-1
14	161.2	29.9	240	5	PCR-US81-06452-1
15	161.2	29.9	340	5	US-09-029-267-13
16	151.4	28.8	798	1	US-07-953-230A-6
17	146	27.1	770	1	US-07-953-230A-1
18	146	27.1	846	1	US-07-953-230A-5
19	118.6	22.0	621	3	US-08-989-251-40
20	118.6	22.0	621	3	US-09-340-250-40
21	118.6	22.0	621	4	US-09-528-108-40
22	110.2	20.4	243	2	US-08-82-182-75
23	109.8	20.4	485	1	US-07-989-845-29
24	109.8	20.4	485	1	US-07-989-844-13
25	109.8	20.4	485	1	US-08-110-663-1
26	109.8	20.4	485	1	US-08-169-688-1
27	109.8	20.4	485	1	US-08-240-121-13

28	109.8	20.4	485	1	US-08-451-241-13	Sequence 13, Appl
29	109.8	20.4	485	1	US-08-110-664-1	Sequence 1, Appl
30	109.8	20.4	485	1	US-08-446-882-1	Sequence 1, Appl
31	109.8	20.4	485	1	US-08-385-187A-1	Sequence 1, Appl
32	109.8	20.4	485	1	US-08-470-108-1	Sequence 1, Appl
33	109.8	20.4	485	5	PCR-US93-11297-13	Sequence 13, Appl
34	109.8	20.4	485	5	PCR-US93-11298-29	Sequence 29, Appl
35	109.2	20.3	237	1	US-07-764-655D-8	Sequence 9, Appl
36	107.6	20.0	237	1	US-07-764-655D-9	Sequence 9, Appl
37	107.6	20.0	717	1	US-08-284-784-40	Sequence 40, Appl
38	107.6	20.0	717	2	US-08-284-784-40	Sequence 40, Appl
39	107.6	20.0	783	1	US-08-854-811-43	Sequence 43, Appl
40	107.6	20.0	783	2	US-08-854-811-43	Sequence 43, Appl
41	107.6	20.0	891	1	US-08-284-784-33	Sequence 33, Appl
42	107.6	20.0	891	1	US-08-284-784-34	Sequence 34, Appl
43	107.6	20.0	891	2	US-08-854-811-33	Sequence 33, Appl
44	107.6	20.0	891	2	US-08-854-811-34	Sequence 34, Appl
45	107.6	20.0	900	1	US-08-284-784-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-142-583A-3
Sequence 3, Appl
Patent No. 6221942

GENERAL INFORMATION:

APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

Query Match 66.2%, Score 356.8; DB 4; Length 553;

Best Local Similarity 82.3%; Pred. No. 1.9e-109;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

QY 1 GGACGAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCTCTTCTGCTGTGTGAGCA 60
DB 31 GGACCGAGAGAGCTGTGGGTGTGAGCTGTGAGCTCTTCTGCTGTGTGAGCA 90
QY 61 AGGGGCTTTTACTTCAACAGCCACAGTATGCTGACAGCATTCGAGAGGACACAG 120
DB 91 AGGGGCTTTTATTCAACAGCCACAGTATGCTGACAGCATTCGAGAGGACACAG 150
QY 121 ACGGCACTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGAGTAC 180
DB 151 ACGGCACTGATGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGAGTAC 210
QY 181 TGTGCTGCTGCAAGCTTACAAAGCTGCTGCTTCCAGGAGGAGGAGGAGGAGGAG 240
DB 211 TGTGAGACCCCTCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 270
QY 241 ATGCCCAAGACTCGAAGTGTGCTGCTTCCGAGCTGTATCTGAGAGGCTGAGAG 300
DB 271 ATGCCCAAGACTCGAAGTGTGCTGCTTCCGAGCTGTATCTGAGAGGCTGAGAG 330
QY 301 AGAGGAAGAGAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
DB 331 AGAGGAAGAGAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 390
QY 361 CAGATGTAGAGAGGAGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 391 CAGATGTAGAGAGGAGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 450
QY 421 CTGCTTGAAGAGCTGCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 480
DB 451 CTGCTTGAAGAGCTGCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 504
QY 481 TCATTTGAGAGATGGGATTTCCCTCAATGAAATACAGAGTAAACATTC 530
DB 505 ACATTTCAAGAT-GGCATTTCCCGCAATGAAATACAGAGTAAACATTC 553

RESULT 2

US-09-142-583A-5
Sequence 5, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: Linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 341..397

US-09-142-583A-5

Query Match 66.2%; Score 356.8; DB 4; Length 553;
Best Local Similarity 82.3%; Pred. No. 1.9e-109;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

QY 1 GGACGAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCTCTTCTGCTGTGTGAGCA 60
DB 31 GGACCGAGAGAGCTGTGGGTGTGAGCTGTGAGCTCTTCTGCTGTGTGAGCA 90
QY 61 AGGGGCTTTTACTTCAACAGCCACAGTATGCTGACAGCATTCGAGAGGACACAG 120
DB 91 AGGGGCTTTTATTCAACAGCCACAGTATGCTGACAGCATTCGAGAGGACACAG 150
QY 121 ACGGCACTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGAGTAC 180
DB 151 ACGGCACTGATGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGAGTAC 210
QY 181 TGTGCTGCTGCAAGCTTACAAAGCTGCTGCTTCCAGGAGGAGGAGGAGGAGGAGGAG 240
DB 211 TGTGAGACCCCTCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 270
QY 241 ATGCCCAAGACTCGAAGTGTGCTGCTTCCGAGCTGTATCTGAGAGGCTGAGAG 300
DB 271 ATGCCCAAGACTCGAAGTGTGCTGCTTCCGAGCTGTATCTGAGAGGCTGAGAG 330
QY 301 AGAGGAAGAGAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
DB 331 AGAGGAAGAGAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 390
QY 361 CAGATGTAGAGAGGAGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 391 CAGATGTAGAGAGGAGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 450
QY 421 CTGCTTGAAGAGCTGCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 480
DB 451 CTGCTTGAAGAGCTGCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 504
QY 481 TCATTTGAGAGATGGGATTTCCCTCAATGAAATACAGAGTAAACATTC 530
DB 505 ACATTTCAAGAT-GGCATTTCCCGCAATGAAATACAGAGTAAACATTC 553

RESULT 3

US-09-142-583A-10
Sequence 10, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/142,583A
 FILING DATE: 29-Oct-1998
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/GB97/00658
 FILING DATE: 11-MAR-1997
 APPLICATION NUMBER: GB 9605124.8
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: SANDOFF, B. J.
 REGISTRATION NUMBER: 36663
 REFERENCE/DOCKET NUMBER: 117-263
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7038164100
 TELEFAX: 7038164100
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 777 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 26..493
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-142-583A-10
 Query Match 50.6%; Score 272.6; DB 4; Length 777;
 Best Local Similarity 75.8%; Pred. No. 3.1e-81;
 Matches 404; Conservative 0; Mismatches 69; Indels 60; Gaps 3;
 QY 1 GGACACAGACCCCTTTGCGGGGCTGAGCTGTGACGACCTTTCAGTTCGTGTGACCA 60
 DB 179 GGACCGGAGACGCTCTCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGAGAC 238
 QY 61 AGGGGCTTTACTTCAACAAGCCACAGCTATGGCTCCAGCATTCGGAGGACACACAG 120
 DB 239 AGGGGCTTTATTTTCAACAAGCCACAGGATATGGCTCCAGCATTCGGAGGACACACAG 298
 QY 121 ACGGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 299 ACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
 QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCAAGTCTTCATCCGAGGCTCCAGGCTCCAGTAC 240
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 QY 419 ATGCCCAAGACCCAG----- 433
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 DB 434 -----AAGGAAGTACATTGGAAGAACGCAAGTAGAGGAGTAGAGAAACAAAGACTA 486
 QY 361 CAGAATGTAGAGAGGCTCCCGAGAAAGAAAGTCCAGCCGACCGAGAGATCCCTTG 420
 DB 487 CAGATATAGAGAGACCTCTCTGAGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 546
 QY 421 --CTGCTTGAAGCAACTGCAAAACATCGAACCTGCCAAATATCAATATGAGTTCAA 478
 DB 547 CTCTGCGAGAGTACCTGTTAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600
 QY 479 TATCATTTGAGATGGGCAATTCCTCATGAAATACAAATACAAATACAAATACAAATTC 531
 DB 601 TATCATTTAAAGATGGGCGTTTCCCAATGAAATACAAATACAAATACAAATTC 653

RESULT 4
 5405942-2
 Patent No. 5405942
 APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
 JAMES P.
 TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
 I AND II
 NUMBER OF SEQUENCES: 16
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/65,673
 FILING DATE: 16-JUN-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 630,557
 FILING DATE: 19-JUL-1984
 SEQ ID NO: 2:
 LENGTH: 622
 5405942-2
 Query Match 50.3%; Score 271; DB 6; Length 622;
 Best Local Similarity 61.2%; Pred. No. 9.4e-81;
 Matches 326; Conservative 77; Mismatches 70; Indels 60; Gaps 3;
 QY 1 GGACACAGACCCCTTTGCGGGGCTGAGCTGTGACGCTTTCAGTTCGTGTGACCA 60
 DB 45 GGACCGGAGACGCTCTCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGAGAC 104
 QY 61 AGGGGCTTTACTTCAACAAGCCACAGCTCTGCTCCAGCATTCGGAGGACACACAG 120
 DB 105 AGGGGCTTTATTTTCAACAAGCCACAGGATATGGCTCCAGCATTCGGAGGACACACAG 164
 QY 121 ACGGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 165 ACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 224
 QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCAAGTCTTCATCCGAGGCTCCAGGCTCCAGTAC 240
 DB 225 TGGCACCCTCAAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 284
 QY 241 ATGCCCAAGACTGAGAGTCCAGCCCTATCGACACACAAGAAAGAAAGTCAAGG 300
 DB 285 ATGCCCAAGACCCAG----- 299
 QY 301 AGAAGAAAGAAAGTACACTTGAAGACAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 360
 DB 300 -----AAGGAAGTACATTGGAAGAACGCAAGTAGAGGAGTAGAGAAACAAAGACTA 352
 QY 361 CAGAATGTAGAGAGGCTCCCGAGAAAGTCCAGCCGACCGAGAGATCCCTTG 420
 DB 353 CAGGAGGAGAGAGGCTCCCGAGAAAGTCCAGCCGACCGAGAGATCCCTTG 412
 QY 421 --CTGCTTGAAGCAACTGCAAAACATCGAACCTGCCAAATATCAATATGAGTTCAA 478
 DB 413 CTCTGCGAGAGTACCTGTTAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 466
 QY 479 TATCATTTGAGATGGGCAATTCCTCATGAAATACAAATACAAATACAAATACAAATTC 531
 DB 467 TATCATTTAAAGATGGGCGTTTCCCAATGAAATACAAATACAAATACAAATTC 519
 RESULT 5
 US-08-472-809B-8
 Sequence 8, Application US/08472809B
 Patent No. 5925364
 GENERAL INFORMATION:
 APPLICANT: Schwartz, Robert J.
 APPLICANT: Dekay, Franco J.
 APPLICANT: O'Malley, Bert W.
 TITLE OF INVENTION: Expression Vector Systems and
 TITLE OF INVENTION: Method of Use
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESS: Lyon & Lyon

QY	_____	GGAGCAGAAACCCCTTTGGGGGGCTGAGCTGGTGGACCCCTCTAGTTCTGTTGTGAGACA	60
Db	793	GGAGCCGGAACACCTCTGGGGGGCTGAGCTGGTGGATGCTTTAGTTCTGTTGTGAGAC	852
QY	61	AGGGGTTTAACTTCACAAAGCCACACTATATGGCTCCAGACATTGGAGGGCACCACAG	120
Db	853	AGGGGTTTATTATTCACAAAGCCACACAGGATATGGCTCCAGCACTGGAGGGCCCTCAG	912
QY	121	ACGGGCAATTGGGATGAGTGTGCTTCCGAGCTGTGATCTGAGGAGGCTGGAGATGAC	180
Db	913	ACGGGCAATCGTAGAGAGAGTGGTGTCTCCGAGCTGTATCTAAGGAGGCTGGAGATGAT	972
QY	181	TGTTGCCGTGGAACGCTACAAAGTCACACTGTTCCATCCGGGCCACAGGCCACACTGAC	240
Db	973	TGGCACCCCTTAACCTCTGCCAAGTCACACTGCTGTCTGCTGCCAGGCCACACAGCAC	1032
QY	241	ATGCCCAAGACTCAAGAACTCCAGGCCCTATCGACACACAAGAAAAGAGCTGCACAAAG	300
Db	1033	ATGCCCAAAACCCAG-----	1047
QY	301	AGAGGAAAGAGATPACACTTTGAAGAACACAAAGTAGAGAAAGTGCAGAGAAACAAGACTA	360
Db	1048	-----AAGGAGATPACATTTGAAGAAACGCAAGTAGAGGAGATGCGAGAGAAACAAGACTA	1100
QY	361	CAGAATGTAGAGAGAGCCCTCCCGAGAGAACGAAAAATGCCAGTCACCAGCAAGATCC	416
Db	1101	CAGGATGTAGAGAGACCTCTCTGAGGATGAAGATGACATGGCCACCGAGGATCT	1156

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Sequence 7 Application US/08472809B
Patent No. 5925564
GENERAL INFORMATION:
APPLICANT: Schwartz, Robert J.
APPLICANT: Demaco J.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Expression Vector Systems and
TITLE OF INVENTION: Method of Use
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-3066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6345 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-7

Query Match 41.2% Score 222; DB 2; Length 6345;
Best Local Similarity 75.5%; Pred. No. 8,7e-64;
Matches 314; Conservative 0; Mismatches 50; Indels 52; Gaps 1

Dy 1 GACACGAGACCCCTTTGGGGGGAGCTGAGCTGGTGGACGCTCTTCAAGTTCGTGTGGACCA 60
Dy 3702 GGACGCGAAGCCCTTCGGGGGGAGCTGAGCTGGTGGATGCTCTTCAAGTTCGTGTGGAC 3761
Dy 61 AGGGGGCTTTAATTAACAAGACCCCAAGTATGCTGCCAGCACTTTGGGGGGGACACAG 120
Dy 3762 AGGGGCTTTATTTTAAACAAGCCCAAGGTATGGCTCCAGCACTGGAGGGGGCTTCA 3821
Dy 121 ACGGGCATTTGGATGAGTGTGCTTGGCTCCGAGCTGTGATCTTGAGAGAGGCTGGAGATGAC 180
Dy 3822 ACAGGCGATGTGATGATGATGCTGCTCCGGAGCTGTATCTTAAGGAGGGCTGGAGATGAT 3881
Dy 181 TGTGTCCGCTGAAGCCCTACAAGATGAGTGTGCTTCCATTCGGGGCCAGGGCCACACTGAC 240
Dy 3882 TGGCGACCCCTTAAAGCTTCCCAAGTCAAGCTGCTCTTCCGTGCCAGGCGCCACACGAC 3941
Dy 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAGAG 300
Dy 3942 ATGCCCAAGACCCAG-- 3956

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APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO: 11
LENGTH: 210
5405942-11

Query Match 30.9%; Score 166.8; DB 6; Length 210;
Best Local Similarity 87.1%; Pred. No. 3.2e-46;
Matches 183; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGACCA 60
DB 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 120
DB 61 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 120
QY 121 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAC 180
DB 121 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAT 180
QY 181 TGTGTCGCTGCAGAGCTTACCAAGTCAGCT 210
DB 181 TGGCGACCCCTCAAGCCTTGCACAGTCAGCT 210

RESULT 11
US-09-255-829-13
Sequence 13, Application US/09255829
Patent No. 6461617

GENERAL INFORMATION:

APPLICANT: Stone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-FEB-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2500

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..2862
US-09-255-829-13

Query Match 30.9%; Score 166.8; DB 4; Length 2862;
Best Local Similarity 87.1%; Pred. No. 1.5e-45;
Matches 183; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGACCA 60
DB 2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGAC 2703
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 120
DB 2704 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 2763
QY 121 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAC 180
DB 2764 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAT 2823
QY 181 TGTGTCGCTGCAGAGCTTACCAAGTCAGCT 210
DB 2824 TGGCGACCCCTCAAGCCTTGCACAGTCAGCT 2853

RESULT 12
5405942-15
Patent No. 5405942

APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER, JAMES P.

TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/65,673

FILING DATE: 16-JUN-1987

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 630,557

FILING DATE: 19-JUL-1984

SEQ ID NO: 15

LENGTH: 210

5405942-15

Query Match 30.6%; Score 165.2; DB 6; Length 210;
Best Local Similarity 87.1%; Pred. No. 1.1e-45;
Matches 141; Conservative 41; Mismatches 28; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGACCA 60
DB 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTCACTTGTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 120
DB 61 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACAG 120
QY 121 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAC 180
DB 121 ACAGGATTCGTGATGATGATGCTTCCGAGAGCTGTGATGAGAGAGCTGAGATGAT 180
QY 181 TGTGTCGCTGCAGAGCTTACCAAGTCAGCT 210
DB 181 TGGCGACCCCTCAAGCCTTGCACAGTCAGCT 210

RESULT 13
US-08-308-196A-1
Sequence 1, Application US/08308196A

GENERAL INFORMATION:

APPLICANT: Briarley, Russell A.
APPLICANT: Davis, Geneva R.
APPLICANT: Holtz, Gregory C.
APPLICANT: Gleeson, Martin A.

```

1  APPLICANT: Bradley, D. H.
2  TITLE OF INVENTION: Production of Insulin-Like Growth
3  TITLE OF INVENTION: Factor-1 in Methylophilic Yeast Cells
4  NUMBER OF SEQUENCES: 12
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Fitch, Even, Tabin & Flannery
7  STREET: 135 South LaSalle Street, Suite 900
8  CITY: Chicago
9  STATE: Illinois
10 COUNTRY: USA
11 ZIP: 60603
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentin Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: PCT/US91/06452
20 FILING DATE: 19910409
21 CLASSIFICATION: 435
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/578,728
24 FILING DATE: 04-SEP-1990
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Seidman, Stephanie L.
27 REGISTRATION NUMBER: 33,779
28 REFERENCE/DOCKET NUMBER: 51874
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (619)552-1311
31 TELEFAX: (619)552-0095
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 240 base pairs
35 TYPE: NUCLEIC ACID
36 STRANDEDNESS: double
37 TOPOLOGY: unknown
38 MOLECULE TYPE: cDNA
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 14..232
42 PCT-US91-06452-1
43
44 Query Match 29.9%; Score 161.2; DB 5; Length 240;
45 Best Local Similarity 84.6%; Pred. No. 2,6e-44;
46 Matches 181; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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48 QY 1 GCACCGAAGACCCCTTGCGGGGCTGAGCTGAGGACGGCTTCAGCTGCTGAGTGGACCA 60
49 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 Db 17 GGACCGGAACCGCTCTGCGGGGCTGAGCTGAGGATGCTTCGACATGTGTGTGGACAC 76
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52 QY 61 AGGGGCTTTACTTCAACAGGCCACAGTCTATGCTCCAGCATTCGGAGGGCACACAG 120
53 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
54 Db 77 AGGGGCTTTATTATTCACAGGCCACAGGGATGAGCTCCAGAGAGTCAGCGGGGCTCAG 136
55
56 QY 121 AGCGGATGTGTGGATGAGTGTGTGCTTCGGAGACTGTATCTGAGAGGCTGGAGATGTAC 180
57 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
58 Db 137 ACAGGATGTGTGATGAGTGTGTGCTTCGGAGACTGTATCTAAGAGAGGCTCGAGATGTAT 196
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60 QY 181 TGTGTCGGTCCAGAGCTTCACAAAGTCAGCTGT 214
61 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 Db 197 TGGGACCCCTCAGAGCTTCAGAGTACAGTCTGAT 230
63
64 RESULT 15
65 US-09-029-267-13
66 ; Sequence 13, Application US/09029267
67 ; Patent No. 6107057
68 ; GENERAL INFORMATION:
69 ; APPLICANT: Crawford, Kenneth
70 ; APPLICANT: Zarot, Isabel
71 ; APPLICANT: Innis, Michael
72 ; TITLE OF INVENTION: Pichia Secretary Leader for Protein
73 ; TITLE OF INVENTION: Expression

```


NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Chung Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

Query Match 29.98; Score 161.2; DB 3; Length 390;
Best Local Similarity 84.6%; Pred. No. 3.4e-44;
Matches 181; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 GSACACAGAGACCTTGGCGGGCTGAGCTGAGACGCTCTCAGTGTGTGTGACCA 60
DB 160 GSACACGAGAGCGCTGCGGGGGCTGAGCTGAGATGCTGCTGCTGTGTGTGAGAC 219
QY 61 AGGGGCTTTACTTCACACAGCCACAGTCTATGCTCCAGCATTCGAGAGGACACACAG 120
DB 220 AGGGGCTTTATTTCACACAGCCACAGGGGTATGCTCCAGCATTCGAGAGGAGCTCAG 279
QY 121 ACGGGCAATTGTGATGATGTTGCTTCGGAGCTGTGATGAGAGGCTGAGATGTAC 180
DB 280 ACAGGCAATGATGATGATGCTGCTCCGAGCTGTGATGAGAGGCTGAGATGTAT 339
QY 181 TGTGTCCGCTGCAAGCTACAAAGTCACTCTT 214
DB 340 TGGCACCCTCTCAAGCTGCCAAGTCACTGTAT 373

Search completed: June 15, 2003, 18:20:41
Job time : 44.5935 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 97.6276 Seconds

(Without alignments)
7994.713 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggaccagagacccttgagg.....agtaaacattcccggaattc 539

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCIT_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	539	100.0	10 US-09-852-261-3	Sequence 3, Appl1
2	453.8	84.2	651 9 US-10-161-088-1	Sequence 1, Appl1
3	425	78.8	487 10 US-09-852-261-11	Sequence 11, Appl1
4	356.8	66.2	523 10 US-09-852-261-5	Sequence 5, Appl1
5	325.2	60.3	517 10 US-09-852-261-1	Sequence 1, Appl1
6	274.2	50.9	7260 9 US-10-136-639-4	Sequence 4, Appl1
7	274.2	50.9	10 US-09-919-497-24	Sequence 24, Appl1
8	274.2	50.9	7260 10 US-09-880-107-3739	Sequence 3739, Ap
9	262	48.6	471 10 US-09-852-261-13	Sequence 13, Appl1
10	213.8	39.7	286 9 US-10-161-088-3	Sequence 3, Appl1
11	205.8	38.4	318 10 US-09-852-261-9	Sequence 9, Appl1
12	205.6	37.8	462 9 US-10-238-114-1	Sequence 1, Appl1
13	164.6	30.5	4532 10 US-09-930-377B-1	Sequence 1, Appl1
14	163.6	30.4	210 10 US-09-930-377B-2	Sequence 13, Appl1
15	161.2	29.9	390 9 US-10-179-046-13	Sequence 9, Appl1
16	124.2	23.0	213 9 US-10-076-816-9	Sequence 9, Appl1
17	124.2	23.0	213 9 US-10-077-381-9	Sequence 9, Appl1
18	118.6	22.0	621 9 US-10-280-826-40	Sequence 40, Appl1
19	118.6	22.0	621 10 US-09-921-398-40	Sequence 40, Appl1

20	105.4	19.6	480 9 US-10-280-826-38	Sequence 38, Appl1
21	105.4	19.6	480 10 US-09-921-398-38	Sequence 38, Appl1
22	67.4	12.5	411 10 US-09-960-352-2082	Sequence 2082, Ap
23	67.2	12.5	437 9 US-10-066-543-663	Sequence 663, App
24	67.2	12.5	493 9 US-10-066-543-997	Sequence 997, App
25	67.2	12.5	518 9 US-10-066-543-1040	Sequence 1040, Ap
26	67.2	12.5	536 9 US-10-066-543-428	Sequence 428, App
27	67.2	12.5	543 9 US-10-136-841-1	Sequence 1, Appl1
28	67.2	12.5	549 9 US-10-066-543-478	Sequence 478, App
29	67.2	12.5	574 9 US-10-025-380-918	Sequence 918, App
30	67.2	12.5	574 10 US-09-922-217-918	Sequence 918, App
31	67.2	12.5	574 10 US-09-833-263-918	Sequence 918, App
32	67.2	12.5	577 9 US-10-066-543-1137	Sequence 1137, App
33	67.2	12.5	579 9 US-10-066-543-1094	Sequence 1094, Ap
34	67.2	12.5	586 9 US-10-066-543-808	Sequence 808, App
35	67.2	12.5	1356 9 US-10-081-119-37	Sequence 37, Appl1
36	67.2	12.5	1356 9 US-10-097-340-144	Sequence 144, App
37	67.2	12.5	1356 10 US-09-962-436-293	Sequence 293, App
38	67.2	12.5	1356 10 US-09-954-456-294	Sequence 294, App
39	67.2	12.5	1356 10 US-09-880-107-2092	Sequence 2092, Ap
40	67.2	12.5	4350 9 US-10-123-181-37	Sequence 37, Appl1
41	66	12.2	854 9 US-09-954-531-989	Sequence 989, App
42	65.8	12.2	447 9 US-10-025-380-917	Sequence 917, App
43	65.8	12.2	447 10 US-09-922-217-917	Sequence 917, App
44	65.8	12.2	447 10 US-09-833-263-917	Sequence 917, App
45	62.4	11.6	237 9 US-10-136-841-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1				
US-09-852-261-3				
Sequence 3, Appl1 Application US/09852261				
Patient No. US20020083477A1				
GENERAL INFORMATION:				
APPLICANT: GOLDSPEINK, GEOFREY				
APPLICANT: TERENCEHI, GIORGIO				
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE				
FILE REFERENCE: 117-351				
CURRENT APPLICATION NUMBER: US/09/852,261				
CURRENT FILING DATE: 2001-05-10				
PRIOR APPLICATION NUMBER: GB 0011278.9				
PRIOR FILING DATE: 2000-05-10				
NUMBER OF SEQ ID NOS: 14				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 3				
LENGTH: 539				
TYPE: DNA				
ORGANISM: Rattus sp.				
US-09-852-261-3				
Query Match				
Best Local Similarity 100.0%; Pred No. 3.9e-171;				
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	GGACCAAGAGACCCCTTGGCGGGCTGAGCTGTGAGACGCTCTTCAGTTCTGTGTGAGACCA	60	
DB	1	GGACCAAGAGACCCCTTGGCGGGCTGAGCTGTGAGACGCTCTTCAGTTCTGTGTGAGACCA	60	
QY	61	AGGGGCTTTTACTTCAACAGCCCAAGCTCTAGCTTCAGATTGGAGGGCACCACAG	120	
DB	61	AGGGGCTTTTACTTCAACAGCCCAAGCTCTAGCTTCAGATTGGAGGGCACCACAG	120	
QY	121	ACGGGATGTGTAGTGTGCTTCGAGACTGTGATGAGAGGCTGAGAGATGTAC	180	
DB	121	ACGGGATGTGTAGTGTGCTTCGAGACTGTGATGAGAGGCTGAGAGATGTAC	180	
QY	181	TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCACTGAC	240	
DB	181	TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCACTGAC	240	
QY	241	ATGCCCAAGACACAGAGTCCAGGCCCTATGACACACAAAGAGAGCTGGAAGG	300	

Db	241	ATGCCCAATCTCAAGATGCCAGCCCTATTCGACACACAGAAAGAAAGAGCTGCAAGG	300
Qy	301	AGAAGCAAGAGAGATACACTTGAACACACAGTAGAGAGAGTAGCAGAAACAGACCTA	360
Db	301	AGAGAGAAAGAGATACACTTGAACACACAGTAGAGAGTAGCAGAAACAGACCTA	360
Qy	361	CAGAAATGTAGGAGAGACCTCCCGAGGAACAGAAAATGCACGCTACCGCAGATCCTTTG	420
Db	361	CAGAAATGTAGGAGAGACCTCCCGAGGAACAGAAAATGCACGCTACCGCAGATCCTTTG	420
Qy	421	CTGCTTTGAGCAACTGCAAAACATGGAACACTGCCAAATATCAATAAAGATTCAATA	480
Db	421	CTGCTTTGAGCAACTGCAAAACATGGAACACTGCCAAATATCAATAAAGATTCAATA	480
Qy	481	TGATTTCAAGATGGGCAATTCCTCCCATGAAATACAAAGTAACAATCCCGGAATTC	539
Db	481	TGATTTCAAGATGGGCAATTCCTCCCATGAAATACAAAGTAACAATTCGCGGAATTC	539

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RESULT 2
US-10-161-088-1
: Sequence 1, Application US/10161088
: Publication NO. US2003007761A1
: GENERAL INFORMATION:
: APPLICANT: Parrot, Venda
: APPLICANT: Rosengren, Linda
: TITLE OF INVENTION: NEW METHODS
: FILE REFERENCE: 13425-111001
: CURRENT FILING DATE: 2002-05-31
: PRIOR APPLICATION NUMBER: US/10/161, 088
: PRIOR APPLICATION NUMBER: SE 0101934-8
: PRIOR FILING DATE: 2001-06-01
: NUMBER OF SEQ IDS: 3
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 651
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (73)..(471)
: US-10-161-088-1

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Query Match	84.28;	Score 453.8;	DB 9;	Length 651;
Best Local Similarity	92.88;	Pred. No. 2.2e-142;		
Matches 476;	Conservative	0;	Mismatches 37;	Indels 0;
				Gaps 0;

OY		GGCAGGAACCCCTTGGCGGGCTAGGCTGGAGGCGCTTTCAGTTGCTGTGTGGACCA	60
Db	139	GGACCGAAGACCCCTTGGCGGGCTAGGCTGGAGGCTTTCAGTTGCTGTGTGGACCG	198
OY	61	AGGGGCTTTACTCTAACAAAGCCACAGCTATGGCTCAGCATTTGGAGGGACCCAG	120
Db	199	AGGGCTTTACTCTACAAAGCCACAGGCTATGGCTCAGCATTTGGAGGGACCCAG	258
OY	121	ACGGGCTTTGGAGTAGTGTGTTCCGGAGCTGTGATCTGAGAGGCTGGAGATGAC	180
Db	259	ACAGGCTTTGGAGTAGTGTGTTCCGGAGCTGTGATCTGAGAGGCTGGAGATGTAC	318
OY	181	TGATGCTGGTGGAAAGCTCAGAAAGTCAGCTGGTTCATCCGGGGCCACGGCCACACTGAC	240
Db	319	TGATGCTGGTGGAAAGCTCAGAAAGTCAGCTGGTTCATCCGGGGCCACGGCCACACTGAC	378
OY	241	ATGCCAGAGACTGAGAGTCCCGCCCTATGACACCAAGAAAGAGACTGCAAAAGG	300
Db	379	ATGCCAGAGACTGAGAGTCCCGCCCTATGACCAAAAGAAAGAGACTGCAAAAGG	438
OY	301	AGAGAGAAAGAGAGTACACTTAAACAAACAAAGTAGAGAGAAAGTCAGGAAACAGACTTA	360
Db	439	AGAGAGAAAGAGAGTACACTTAAACAAACAAAGTAGAGAAAGTCAGGAAACAGACTTA	498
OY	361	CAGGATGTGGAGGAGGCTCCCGGAGGAACAGAAATGCTCAGCTACCGCAAGATCTTTTG	420

Db	499	CAGAAATGTGAGAGAGAACCTCCACCGSAGACAGAAATGGCCATCCACCGCAGATCCTTG	558
Qy	421	CTGCTTGAGCAACCTGCAAAACATGTGGACACCTGCCAATATGTAATATGAGCTTCATA	480
Db	559	CTGCTTGAGCAACCTGCAAAACATGTGGACACCTGCCAATATGTAATATGAGCTTCATA	618
Qy	481	TCATTTCAGAGATGGGCAATTCCTCCATCGATAA	513
Db	619	ACATTACAAGATGGGCAATTCCTCCATCGATAA	651

RESULT 3
 US-09-852-261-11
 : Sequence 11, Application US/09852261
 : Patent No. US20020083477A1
 : GENERAL INFORMATION:
 : APPLICANT : GOLDSPIRK, GEOFFREY
 : APPLICANT : TENENHINK, GIORGIO
 : TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
 : FILE REFERENCE: 117-351
 : CURRENT APPLICATION NUMBER: US/09/852,261
 : CURRENT FILING DATE: 2001-05-10
 : PRIOR APPLICATION NUMBER: GB 0011278.9
 : PRIOR FILING DATE: 2000-05-10
 : NUMBER OF SEQ. ID NOS: 14
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO. 11
 : LENGTH: 487
 : TYPE: DNA
 : ORGANISM: Rattus sp.
 : US-09-852-261-11

Query Match	78.8%	Score 425	DB 10	Length 487
Best Local Similarity	90.4%	Pred. No.	9,4e+133	
Matches 487	Conservative 0	Mismatches 0	Indels 52	Gaps 1

OY	61	AGGAGCTTTTACTTCAACAAGCCCAAGTCTATGAGTCTCAGACATTGCGAGGACACACAG	120
Db	61	AGGGGGTTTTTACTTCAACAAGCCCAAGTCTATGAGTCTCAGACATTGCGAGGACACACAG	120
OY	121	ACGGAGCATTTGGATAGTGTGTCTTCCGAGACTTGATCTGAGAGAGCTGGAGATGTAC	180
Db	121	ACGGGCAATTGTGATAGTGTGTCTTCCGAGACTGTATCTGAGAGAGCTGGAGATGTAC	180
OY	181	TGTGTCCGCTGCAAGCTCTCAAAAGTCAAGTGTCTTCATCCGGGCCACAGCCACACTGAC	240
Db	181	TGTGTCCGCTGCAAGCTCTCAAAAGTCAAGTGTCTTCATCCGGGCCACAGCCACACTGAC	240
OY	241	ATGCCCAAGACTCAGAGTCCCAAGCCCATCGATCGACACACAAGAAAAGAAAGCTGGCAAGG	300
Db	241	ATGCCCAAGACTAG-----	255
OY	301	AGAAAGAAAGAAAGTACACTTGAAGACACAAAGTATGAGGAAGTCCAGAAAACAAGACTTA	360
Db	256	-----AAGGAAGTACACTTGAAGAAACAAGTATGAGGAAGTCCAGAAAACAAGACTTA	308
OY	361	CAGATGTATGAGGAGACCTCCGAGSAAACAGAAAATGTCACGTACCGCAAGATCCTTTG	420
Db	309	CAGATGTATGAGGAGACCTCCGAGSAAACAGAAAATGTCACGTATCCGCAAGATCCTTTG	368
OY	421	CTGCTTGAACAACCTTGCAAAACATCGSAAACCTGCCAAATATCAATATATGAGTTCAATA	480
Db	369	CTGCTTGAACAACCTTGCAAAACATCGSAAACCTGCCAAATATCAATATATGAGTTCAATA	428
OY	481	TCATTTCAAGATGGGCAATTTCCCTCATGGAATACAAATTAACATTTCCCGGAATTC	539
Db	429	TCATTTCAAGATGGGCAATTTCCCTCAATGGAATACAAATTAACATTTCCCGGAATTC	487

RESULT 5
US-09-852-261-1
: Sequence 1, Application US/09852261
: Patent No. US20020083477A1
: GENERAL INFORMATION:
: APPLICANT: GOLDSPIRK, GEOFFREY
: APPLICANT: TERENCEH, GEORGE
: TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
: FILE REFERENCE: 117-351
: CURRENT APPLICATION NUMBER: US/09/852, 261

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1 CURRENT APPLICATION NUMBER: US/10/136,639-4
2 CURRENT FILING DATE: 2002-09-06
3 PRIOR APPLICATION NUMBER: US 60/329,650
4 PRIOR FILING DATE: 2001-10-16
5 NUMBER OF SEQ ID NOS: 4
6 SOFTWARE: PatentIn version 3.0
7 SEQ ID NO 4
8 LENGTH: 7260
9 TYPE: DNA
10 ORGANISM: Homo sapiens
11 US-10-136-639-4

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Query Match 50.9%: Score 274.2; DB 9; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAGAGACCCCTTGGGGGGCTGAGCTGTGAGACGCTCTTCAGTTGCTGTGAGACCA 60
DB 311 GGACCAGAGACGCTGTGGGGGGCTGAGCTGTGAGAGTGTCTTCAGTTGCTGTGAGAC 370

QY 61 AGGGGCTTTTACTTAAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACACCAAG 120
DB 371 AGGGGCTTTTATTAAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACGCTCAG 430

QY 121 AGGGGCTTTTGTGATGAGTGTGCTTCCGAGCTGTATGAGAGGCTGGAAGTGTAC 180
DB 431 AGAGCATGCTGTGATGAGTGTGCTTCCGAGCTGTATGAGAGGCTGGAAGTGTAC 490

QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCAAGTCTGCTTCCAGCTCCGAGGCTGCACTGAC 240
DB 491 TGTGTCCGCTTAAACCTTCCAAAGTCAAGTCTGCTTCCAGCTCCGAGGCTGCACTGAC 550

QY 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACAGAAAGAAAGAGTGAAG 300
DB 551 ATGCCCAAGACCCAG----- 565

QY 301 AGAAGAAAGAGTACACTGTAGAGACAAAGTATGAGAGAGTGCAGAAACAGACCTA 360
DB 566 -----AAGGAAGTACATTTGAAAGACAGCAGTATGAGAGAGTGCAGAAACAGACCTA 618

QY 361 CAGAAATGTAGAGAGGCTCCGAGAGAAAGAAATGCGACAGTCCGCAAGATCCTTG 420
DB 619 CAGGATGTAGAGAGGCTCCGAGAGAGTGAAGATGACATGCGCCAGAGATCCTTG 678

QY 421 --CTGCTTGAGCAACCTGCAAAACATCGGAACCTGCGCAATATCAATTAATGATTC 478
DB 679 CTCTGACAGAGTACCTGTGTAACCTTGAACACCTACCA-----AAAAATAGTTTGA 732

QY 479 TATCATTTCAAGATGAGGATTTCCCTCAATGAATTAACAGATTAACATTC 531
DB 733 TAAACATTTAAAGATGAGGCTTCCCAATGAATTAACAGATTAACATTC 785

RESULT 7
US-09-919-497-24
Sequence 24, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 24
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-24

Query Match 50.9%: Score 274.2; DB 10; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAGAGACCCCTTGGGGGGCTGAGCTGTGAGACGCTCTTCAGTTGCTGTGAGACCA 60
DB 311 GGACCAGAGACGCTGTGGGGGGCTGAGCTGTGAGATGCTTCAGTTGCTGTGAGAC 370

QY 61 AGGGGCTTTTACTTAAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACACCAAG 120
DB 371 AGGGGCTTTTATTCAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACGCTCAG 430

QY 121 ACAGGCAATGTGATGAGTGTCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC 180
DB 431 ACAGGCAATGTGATGAGTGTCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAT 490

QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCAAGTCTGCTTCCAGCTCCGAGGCTGCACTGAC 240
DB 491 TGTGTCCGCTTCAAGCTTACAAAGTCAAGTCTGCTTCCAGCTCCGAGGCTGCACTGAC 550

QY 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACAGAAAGAAAGAGTGAAG 300
DB 551 ATGCCCAAGACCCAG----- 565

QY 301 AGAAGAAAGAGTACACTGTAGAGACAAAGTATGAGAGAGTGCAGAAACAGACCTA 360
DB 566 -----AAGGAAGTACATTTGAAAGACAGCAGTATGAGAGAGTGCAGAAACAGACCTA 618

QY 361 CAGAAATGTAGAGAGGCTCCGAGAGAAAGAAATGCGACAGTCCGCAAGATCCTTG 420
DB 619 CAGGATGTAGAGAGGCTCCGAGAGAGTGAAGATGACATGCGCCAGAGATCCTTG 678

QY 421 --CTGCTTGAGCAACCTGCAAAACATCGGAACCTGCGCAATATCAATTAATGATTC 478
DB 679 CTCTGACAGAGTACCTGTGTAACCTTGAACACCTACCA-----AAAAATAGTTTGA 732

QY 479 TATCATTTCAAGATGAGGATTTCCCTCAATGAATTAACAGATTAACATTC 531
DB 733 TAAACATTTAAAGATGAGGCTTCCCAATGAATTAACAGATTAACATTC 785

RESULT 8
US-09-880-107-3739
Sequence 3739, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3739
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

Query Match 50.9%: Score 274.2; DB 10; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAGAGACCCCTTGGGGGGCTGAGCTGTGAGACGCTCTTCAGTTGCTGTGAGACCA 60
DB 311 GGACCAGAGACGCTGTGGGGGGCTGAGCTGTGAGATGCTTCAGTTGCTGTGAGAC 370

QY 61 AGGGGCTTTTACTTAAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACACCAAG 120
DB 371 AGGGGCTTTTATTCAACAAGCCCACTATGAGCTCCAGCATTCGAGAGGACGCTCAG 430

QY 121 ACAGGCAATGTGATGAGTGTGCTTCCGAGCTGTATGAGAGGCTGGAAGTGTAC 180
DB 431 ACAGGCAATGTGATGAGTGTGCTTCCGAGCTGTATGAGAGGCTGGAAGTGTAT 490

QY 181 TGTGTCCGCTGCAAGCTTACAAAGTCAAGTCTGCTTCCAGCTCCGAGGCTGCACTGAC 240

DB 491 TGCCACACCCCTCAGACCTGCGAATGACGCTGCTCCGTGCGCCGCCACACCGAC 550
QY 241 ATGCCCAAGACTCAGAACTCCAGCCCTATCGACACACAGAAAGAAAGCTGCAAGG 300
DB 551 ATGCCCAAGACCCAG-----565
QY 301 AGAAGAAAGAAATACACTTGAAGACAGAGTAGAGAGAGAGAGAGAGAGAGAGACTA 360
DB 566 -----AAGAAATACACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACTA 618
QY 361 CAGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 619 CAGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
QY 421 --CTGCTTGACAGACCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
DB 679 CTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
QY 479 TATCATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
DB 733 TATCATTTAAAGATGGGCGGTTCCCGCATTAAGATGAAGATGAAGATGAAGATTC 785

RESULT 9
US-09-852-261-13
Sequence 13, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFREY
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 13
LENGTH: 471
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

Query Match 48.6%; Score 262; DB 10; Length 471;
Best Local Similarity 74.7%; Pred. No. 7.7e-78;
Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

QY 1 GGACCAAGAGACCCCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1 GGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 AGGAGCTTTTACTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 AGGAGCTTTTATTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 AGGAGCTTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 ACAGGCAATCGTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 180
QY 181 TGTGTCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 TGTGTCACCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 ATGCCCAAGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 ATGCCCAAGACTCAG-----255
QY 301 AGAAGAAAGAAATACACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACTA 360
DB 256 -----AAGAAATACACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACTA 308

QY 361 CAGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 309 CAGAGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
QY 421 CTGCTTGACAGACCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 369 CTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
QY 481 TCATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 530
DB 423 ACATTTCAAAGAT-GGCATTTCCCGCAATGAATACAGAGATGAAGATTC 471

RESULT 10
US-10-161-088-3
Sequence 3, Application US/10161088
Publication No. US2003007761A1
GENERAL INFORMATION:
APPLICANT: Parrow, Vendela
TITLE OF INVENTION: NEW METHODS
FILE REFERENCE: 13425-111001
CURRENT APPLICATION NUMBER: US/10/161,088
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: SE 0101934-8
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 286
TYPE: DNA
ORGANISM: Homo sapiens
US-10-161-088-3

Query Match 39.7%; Score 213.8; DB 9; Length 286;
Best Local Similarity 89.5%; Pred. No. 1e-61;
Matches 230; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TCGGGGCTGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75
DB 18 TCGGGGCTGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 77
QY 76 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
DB 78 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 137
QY 136 GAGTGTGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
DB 138 GAGTGTGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 197
QY 196 CCTACAAAGTACAGCTGCTTCCATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
DB 198 CCTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 257
QY 256 AAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 272
DB 258 GCATGCAAGCTGTCTC 274

RESULT 11
US-09-852-261-9
Sequence 9, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFREY
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 318
TYPE: DNA
ORGANISM: Homo sapiens
US-09-852-261-9

Query Match
Best Local Similarity 38.4%; Score 206.8; DB 10; Length 318;
Matches 226; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGACCA 60
DB 1 GGACCCGAGACGCTGCGGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGAC 60
QY 61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATAGCTCCAGATTCGAGGGGACCAACAG 120
DB 61 AGGGGCTTTTATTTCACAAGCCCAAGGATAGGCTCCAGAGTGGAGGGGCTGACAG 120
QY 121 ACAGGATTTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAC 180
DB 121 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAT 180
QY 181 TGTGTCGCTGCAAGCTTCAAGAGTACCTGTTCCATCCGGGCCACGCTACACTGAC 240
DB 181 TGGCGACCCCTCAAGGCTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATGCCCAAGACTCAGAG 258
DB 241 ATGCCCAAGACCCAGAG 258

RESULT 12

US-10-238-114-1
Sequence 1, Application US/10238114
Publication No. US20030100073A1
GENERAL INFORMATION:
APPLICANT: Merital
APPLICANT: ANDREONI, Christine Michele
TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE RE
FILE REFERENCE: 454313-3165.1
CURRENT APPLICATION NUMBER: US/10/238,114
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: FR 01 11736
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/318,666
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 462
TYPE: DNA
ORGANISM: Felis catus
US-10-238-114-1

Query Match
Best Local Similarity 37.8%; Score 203.6; DB 9; Length 462;
Matches 224; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGACCA 60
DB 145 GGACCAAGACCCCTTGGCGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGACCA 204
QY 61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATAGCTCCAGATTCGAGGGGACCAACAG 120
DB 205 AGGGGCTTTTATTTCACAAGCCCAAGGATAGGCTCCAGAGTGGAGGGGCTGACAG 264
QY 121 ACAGGATTTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAC 180
DB 265 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAC 324
QY 181 TGTGTCGCTGCAAGCTTCAAGAGTACCTGTTCCATCCGGGCCACGCTACACTGAC 240

DB 325 TGTGACCCCTCAAGCCCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
QY 241 ATGCCCAAGACTCAGAG 258
DB 385 ATGCCCAAGGCTCAGAG 402

Query Match
Best Local Similarity 30.5%; Score 164.6; DB 10; Length 4532;
Matches 185; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

US-09-930-377B-1
Sequence 1, Application US/09930377B
Patent No. US20020144296A1
GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Bleck, Gregory T.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: alpha-LA/IGF-I
US-09-930-377B-1

Query Match
Best Local Similarity 84.5%; Pred. No. 1,8e-44;
Matches 185; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGACCA 60
DB 2046 GGACCAAGACCCCTTGGCGGGCTGAGCTGTGGAGCTCTTCACTGCTGTGAGAC 2105
QY 61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATAGCTCCAGATTCGAGGGGACCAACAG 120
DB 2106 AGGGGATTTTATTTCACAAGCCCAAGGATAGGCTCCAGAGTGGAGGGGCTGACAG 2165
QY 121 ACAGGATTTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAC 180
DB 2166 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATCGAGAGGCTGAGATGTAT 2225
QY 181 TGTGTCGCTGCAAGCTTCAAGAGTACCTGTTCCATC 219
DB 2226 TGGCGACCCCTCAAGGCTTCCCAAGTCACTGATGATGCTC 2264

RESULT 14

US-09-930-377B-2
Sequence 2, Application US/09930377B
Patent No. US20020144296A1
GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 210

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1146.61 Seconds
(without alignments)
7613.181 Million cell updates/sec

Title: US-09-852-261-3
Perfect score: 539
Sequence: 1 ggacacagacaccccttcgg.....agtaacatcccggaattc 539

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estb1:*
2: em_estb2:*
3: em_estb3:*
4: em_estb4:*
5: em_estb5:*
6: em_estb6:*
7: em_estb7:*
8: em_estb8:*
9: em_estb9:*
10: em_estb10:*
11: em_estb11:*
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13: em_estb13:*
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25: em_estb25:*
26: em_estb26:*
27: em_estb27:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	501.6	93.1	549	9	A1169253 EST215088
2	469.2	87.1	558	9	A1503976 vnt33d08.x
3	453.4	84.1	623	10	AM146128 um37e10.x
4	450.4	83.6	468	9	A1169770 EST215669
5	446.8	82.9	558	9	A1268629 u04b07.x
6	437	81.1	653	14	BQ200567 U1-R-D21-BQ200567

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	GENE INDEX	COMMENT	FEATURES
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779

ALIGNMENTS

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	GENE INDEX	COMMENT	FEATURES
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779
A1169253	EST215088	Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone	A1169253	1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R. and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.	Other ESTs: TC50779

```

source
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/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RK18P33"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: p713pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT      112 a      140 c      133 g      164 t
ORIGIN

Query Match      93.1%; Score 501.6; DB 9; Length 549;
Best Local Similarity 97.3%; Pred. No. 2e-18;
Matches 510; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      8 AGACCTTTGGGGGCTGAGCTGTGAGAGCTCTCACTGTCTGTGTGACCAAGGGCT 67
Db      549 AGACCTTTGGGGGCTGAGCTGTGAGAGCTCTCTCACTGTGTGTGACCAAGGGCT 490
QY      68 TTACTTCAACAAGCCACAGCTGTAGGCTCCAGATTGGAGGGCACACAGAGGCA 127
Db      489 TTACTTCAACAAGCCACAGCTGTAGGCTCCAGATTGGAGGGCACACAGAGGCA 430
QY      128 TTGTGATGAGTGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTCTGTTC 187
Db      429 TTGTGATGAGTGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTCTGTTC 370
QY      188 GCTGCAAGCTCAAAAGTCAAGTCTGCTTCATCCGGGCGCCAGCCACATGACATGCCA 247
Db      369 GCTGCAAGCTCAAAAGTCAAGTCTGCTTCATCCGGGCGCCAGCCACATGACATGCCA 310
QY      248 AGACTCAGAGTCCCAAGCTTATGACACACAAAGAAAGAAAGTCCAAAGAGAGA 307
Db      309 AGACTCAGAGTCCCAAGCTTATGACACACAAAGAAAGAAAGTCCAAAGAGAGA 250
QY      308 AAGGAAGTCACTTGTAGAGACACAAGTAGAGAGAGAGAGAGAGAGAGAGAG 367
Db      249 AAGGAAGTCACTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
QY      368 TAGGAGAGAGCTCCGAGAGACAAATGCCAGCTCACCGAGATCTTGTGCTTG 427
Db      189 TAGGAGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
QY      428 AGCAACTGCAAAACATCGAGACACCTGCAATATGATATGATGATCAATATTC 487
Db      129 AGCAACTGCAAAACATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
QY      488 AGAGATGGGCAATTTCCCTCAATGAATACACAAGTAACATTC 531
Db      69 AGAGATGGGCAATTTCCCTCAATGAATACACAAGTAACATTC 26

RESULT 2
A1503976/c      558 bp      mRNA      linear      EST 11-MAR-1999
LOCUS      vm43d08.x1 Stratiogene mouse diaphragm (#937303) Mus musculus cDNA
DEFINITION      clone IMAGE:1001007 3' similar to gb:U04482 Mouse mRNA for
                  preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION      A1503976
VERSION      A1503976.1 GI:4401827
KEYWORDS      EST.
SOURCE      Mus musculus
              house mouse.
ORGANISM      Mus musculus
              Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 558)
AUTHORS      Maria M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
              Underwood, K., Steptoe, K., Thelking, B., Allen, M., Bowers, T., Person
              , B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Ritter
              , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
              Waterston, R. and Wilson, R.
              The WashU-NCI Mouse EST Project 1999
              Unpublished (1999)
COMMENT      Contact: Maria M/WashU-NCI Mouse EST Project 1999

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:565223
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 440.
location/Qualifiers
1. 558
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1001007"
/clone_lib="Stratiogene mouse diaphragm (#937303)"
/tissue_type="diaphragm"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
prepared from diaphragm muscle. Primer: 0119c dt. Average
insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACAG 3' -3' adaptor sequence: 5'
CTCGAGTCTTTTCTTTTCTTTT 3'"

BASE COUNT      103 a      133 c      149 g      173 t
ORIGIN

Query Match      87.1%; Score 469.2; DB 9; Length 558;
Best Local Similarity 92.8%; Pred. No. 119;
Matches 492; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY      1 GGACAGAGAGACCCCTTGGGGGCTGAGCTGTGAGAGCTCTTCACTGTGTGTGACCA 60
Db      530 GGACAGAGAGACCCCTTGGGGGCTGAGCTGTGAGATCTTCACTGTGTGTGACCG 471
QY      61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGAGCTCCAGATTCGGAGGACACAG 120
Db      470 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGAGCTCCAGATTCGGAGGACACAG 411
QY      121 AGGGGCTTTGATGATGATGTGTGCTTCCGAGCTGTGATCTGAGAGAGAGAGATGAT 180
Db      410 ACAGGCAATTTGATGATGATGTGTGCTTCCGAGCTGTGATCTGAGAGAGAGATGAT 351
QY      181 TGTGTCCGCTGCAAGCCCTACAAAGTCAAGTCTGTCATCCGAGGCCACGACACTGAC 240
Db      350 TGTGCCCACTGAGAGCTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 291
QY      241 ATGCCCAAGATCTGAGAGTCCGAGCCCTATCCAGACACAGAAAGAGAGAGAGAG 300
Db      290 ATGCCCAAGATCTGAGAGTCCGAGCCCTATCCAGACACAGAAAGAGAGAGAGAG 231
QY      301 AGAAGGAAGGAAGTACACTTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      230 AGAAGGAAGGAAGTACACTTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 171
QY      361 CAGATGTAGAGAGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      170 CAGATGTAGAGAGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 111
QY      421 CTGCTTGAAGCACTGCAAAACATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      110 CTGCTTGAAGCACTGCAAAACATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 51
QY      481 TCATTTAGAGATGGCAATTTCCCTCAATGAATACACAAGTAACATTC 530
Db      50 ACATTTAAGAGATGGCAATTTCCCTCAATGAATATCAAGTAACATTC 1

RESULT 3
AW146128/c      623 bp      mRNA      linear      EST 10-OCT-2000
LOCUS

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DEFINITION	337E10.X1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2247498.3', similar to gb:XM4462 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.			
ACCESSION	AF146128.1 GI:6167864			
VERSION	EST.			
KEYWORDS	house mouse.			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 623) Marrin,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,R., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swallier,T., Gibbons,M., Pape,D., Harey,N., Schur,R., Riltter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Westerman,R. and Wilson,R. The MasRU-NCI Mouse EST Project 1999 Unpublished (1999)			
TITLE	Contact: Maria M/MasRU-NCI Mouse EST Project 1999			
JOURNAL	Washington University School of Medicine			
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1006958 Seq primer: custom primer used High quality sequence stop: 499.			
FEATURES	Location/Qualifiers			
SOURCE	1..623			
	/organism="Mus musculus"			
	/strain="C57BL"			
	/db_xref="taxon:10090"			
	/clone="IMAGE:2247498"			
	/clone_lib="Sugano mouse embryo mewa"			
	/dev_stage="embryo, 14 dpc"			
	/lab_host="DH10B"			
	/note="Vector: pME18S-FLU3; Site.1: DraIII (CACTGTGTC); Site.2: DraIII (CACCATATG); 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCCATTTTATTTTATTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCGTCACTGTCG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector.(3' site CACTGTGTC, 3' site CACCATATG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTTGGCTTAAGAATGCG and 3' end primer CGACTCGACGCTCAGCACA."			
BASE COUNT	123 a 138 c 170 g 191 t 1 others			
ORIGIN				
Query Match	84.1%; Score 453.4; DB 10; Length 623;			
Best Local Similarity	92.1%; Pred. No.5,1e-115;			
Matches	489; Conservative 0; Mismatches 41; Indels 1; Gaps 1			
QY	1 GCACCAAGAACCCCTTTGGGGGCTGAGCTGATGAGCGCTTTTCAATGTTCTGTGTGACCA 60			
DB	541 GGACCAAGAACCCCTTTGGGGGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 482			
QY	61 AGAGGCTTTTACTTAAACAGCCCAAGCTATGATGCTGCAGCACTTGGAGGGGACCAACAG 120			
DB	481 AGAGGCTTTTACTTAAACAGCCCAAGCTATGATGCTGCAGCACTTGGAGGGGACCACTGAG 422			
QY	121 ACAGGCTTTTGTGATGATGATGCTTCCGAGACTGTATGTAGAGGAGGCTGAGATGTAC 180			
DB	421 ACAGGCTTTTGTGATGATGATGCTTCCGAGAGTGTATGTAGAGGAGACTGTGAATGTAC 362			
QY	181 TGTGTCCGCTGACAGCTTACAAAGACAGCTGTTCATTCGAGGGCCAGAGGCCACACTGAC 240			
DB	361 TGTGTCCGCTTACAGCTTACAAAGACAGCCGCGCTCTATTCGTTGCCAGAGCCACATGTAC 302			

QY	241	ATGGCCAAAGCTCAGAAGTCCGACGCCCTATGACACAAAGAAAGAGACCTGCAAGG	300
Db	301	ATGGCCAAAGCTCAGAAGTCCCGTCCCTATGACAAACAGAAAGACAGCTGCAAGG	24
QY	301	AGAAGGAAGGAGTACCTTGAGAACAACAAGTAGAGAAAGTCGAGGAAACAAGCCTA	360
Db	241	AGAAGGGAAGGAGTACCTTTGAGAACCCAAAGTAGAGGAAGTCGAGGAAACAAGCCTA	182
QY	361	CAGAAATATGAGAGACCTCCGAGGAACAGAAATGCAAGTCCACGCAAGATCTTTG	420
Db	181	CAGAAATATGAGAGAGCTCCACGAGGACAGAAATGCACTCCGCGGAGATCTTTG	122
QY	421	CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCCAATATCAATATAGTGTTCATA	480
Db	121	CTGCTTGAGCAACCTGCAAAACATGCAAAACCCCTACCAATATACATATATAGTCCATA	62
QY	481	TCATTTAGAGATGGGCAATTTCCCTCAATGAATAACAAAGAAACATTCG	531
Db	61	ACATTTACAAAGATGGGCAATTTCCG -CAATGAATATATCAAGTAATCAATTCG	12

LOCUS	1169770/c	468 bp	mRNA	linear	EST 20-JAN-1998
DEFINITION	EST215666 Normalized rat liver; Bonto Soares Rattus sp. cDNA clone				
ACCESSION	U01077.3				
VERSION	U01077.3				
KEYWORDS	EST				
SOURCE	Rattus sp.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
REFERENCE	1 (bases 1 to 468)				
AUTHORS	Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.				
TITLE	Rat Genome Project: Generation of a Rat EST (NEST) Catalog & Rat Gene Index				
JOURNAL	Unpublished (1998)				
COMMENT	Other-ESTs: TC50779 Contact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.				
FEATURES	Location/Qualifiers				
source	1. 468 /organism="Rattus sp." /db_xref="ATCC (Inhost):2027570" /db_xref="taxon:10118" /clone="RLR107" /clone_11b="Normalized rat liver, Bonto Soares" /note="Organ: liver; Vector: pT7SPac; Site_1: EcoRI; Site_2: NotI"				
BASE COUNT	85 a 115 c 119 g 149 t				
ORIGIN					
Query Match	83.6%; Score 450.4; DB 9; Length 468;				
Best Local Similarity	97.6%; Pred No. 3,1e-114;				
Matches 457; Conservative	0; Mismatches 11; Indels 0; Gaps 0				
Db	63 GGGCTTTACTGACACAGCCACAGTGTATGGCTCCAGCAFTTGGAGGCGCACACAGAC 1222				
Oy	468 GGGCTTTACTGACACAGCCACAGGCTATGGCTCCAGCAFTTGGAGGCGCGACACAGAC 409				
Db	123 GGGCATTTGGATGAGTGTGTGCTCCGAGGCGTATGTGAGAGGCGTGAAGATGTACTG 1822				
Oy	408 GGGCATTTGGATGAGTGTGTGCTCCGAGGCGTATGTGAGAGGCGTGAAGATGTACTG 349				

OY		183	TGTCCTCCGTCAAGACCTTACAAGTAGCAGCTCGTTCCATCCGGGCCACGCACACTGACT	242
Dd		348	TGTCCTCGTGAAAGCTTACAAGTAGCAGCTCGTTCCATCCGGGCCACGCACACTGACT	289
OY		243	GCCCAAGATCTCAAAGTCCCAGCCCCCTTATGACACACAGAAAAAGAGCTGCAAAAGAG	302
Dd		288	GCCCAAGATCTCAAAGTCCCAGCCCCCTTATGACACACAGAAAAAGAGCTGCAAAAGAG	229
OY		303	AAGAAGAGAAATACTAATTGAAGAAACAAAGTAAGAGAAATGCAGAGAACAGACTACA	362
Dd		228	AAGAAGAGAAATACTAATTGAAGAAACAAAGTAAGAGAAATGCAGAGAACAGACTACA	169
OY		363	GAATGTAGAGAGAGCCTCCCGAGGACACAGAAATGCCAGCTCACCGCAAGTCTTGGT	422
Dd		168	GAATGTAGAGAGAGAGCCTCCCGAGGACACAGAAATGCCAGCTCACCGCAAGTCTTGGT	109
OY		423	GCTTGAGCAACTGCGAAACATCGGAACACTGCCAAATATCAATATATGATGATCATATC	482
Dd		108	GCTTGAGCAACTGCGAAACATCGGAACACTGCCAAATATCAATATATGATGATCATATC	49
OY		483	ATTTCAGAGATGGGCATTTCCCTCAATGAATATACACAGATTAACATTC	530
Dd		48	ATTTCAGAGATGGGCATTTCCCTCAATGAATATACACAGATTAACATTC	1
RESULT 5				
AI265629/c				
LOCUS	AI265629	558 bp	mRNA	linear EST 18-NOV-1996
DEFINITION	UJ0407.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1890901 3' similar to gp.X04482 Mouse mRNA for Preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.			
ACCESSION	AI265629			
VERSION	AI265629.1	GI:3883787		
KEYWORDS	EST			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 558)			
AUTHORS	Marr,M., Hillier,T., Allen,M., Bowles,B., Dietlich,N., Dubouque,T., Giesel,S., Kuba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelning,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston.R.			
TITLE	The WashU-HMT Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMT Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:97525			
FEATURES	Seq primer: custom primer used. High quality sequence scop: 4/5.			
SOURCE	Location/Qualifiers			
	1..558			

Query Match	82.9%	Score 446.8	DB 9	Length 558
Best Local Similarity	92.7%	Pred. No. 3,36-113		
Matches 469	Conservative 0	Mismatches 37	Indels 0	Gaps 0
1	GGACCAGAGACCCCTTGGGGGGGAGTGGTGGACCTCTTCAGTTCGTGTGGACCA	60		
Db	506 GGACCAGAGACCCCTTGGGGGGGAGTGGTGGACCTCTTCAGTTCGTGTGGACCG	447		
QY	61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCACAGTCGAGGGGCAACCA	120		
Db	446 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCACAGTCGAGGGGCAACCA	387		
QY	121 ACGGGCATTTGGATGAGTGTGTTCTCCGAGCTGTGTATCTGAGGAGGCTGGACATGAC	180		
Db	386 ACAGGCATTTGGATGAGTGTGTTCTCCGAGCTGTGTATCTGAGGAGGCTGGACATGAC	327		
QY	181 TGTGTCGGCTCCAGAGCCCAACAAGTCTGAGTGTGTCGAGGGGCAAGCCAGACTGAC	240		
Db	326 TGTGTCGGCTCCAGAGCCCAACAAGTCTGAGTGTGTCGAGGGGCAAGCCAGACTGAC	267		
QY	241 ATGCCCAAGACTCGAAGTCTCCAGCCCTATGACACACACAAGAAAGAGACTGCAAGG	300		
Db	266 ATGCCCAAGACTCGAAGTCTCCAGCCCTATGACACACACAAGAAAGAGACTGCAAGG	207		
QY	301 AGAAGGAAGAAATATGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTG	360		
Db	206 AGAAGGAAGAAATATGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTG	147		
QY	361 CAGATGTAGGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTG	420		
Db	146 CAGATGTAGGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTG	87		
QY	421 CTGCTTGGACCACTGCAAAACATGGAACACCTGCAAAATATATATATATATATATAT	480		
Db	86 CTGCTTGGACCACTGCAAAACATGGAACACCTGCAAAATATATATATATATATATAT	27		
QY	481 TCATTTGAGATGGGATTTTCCCTTC	506		
Db	26 ACATTTGAGATGGGATTTTCCCTTC	1		

BASE COUNT 106 a 135 c 156 g 161 t

ORIGIN

Query Match 82.9% Score 446.8; DB 9; Length 558;
Best Local Similarity 92.7%; Pred. No. 3,36-113;
Matches 469; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

and cloned into distinct DraIII sites of the pHEIS-FR3 vector (5' site CACGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTTAAGCTCGG and 3' end primer CGACCTCGACCTCGACACA."

RESULT 6
BQ200567/c
LOCUS BQ200567 653 bp mRNA linear EST 02-MAY-2002
DEFINITION U1-R-D21-one-a-18-0-U1 s1 U1-R-D21 Rattus norvegicus cDNA clone
U1-R-D21-one-a-18-0-U1 3', mRNA sequence.
ACCESSION BQ200567
VERSION BQ200567.1 GI:20417032
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 653)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized cartilaginous tumor library cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-43,
>AT-rich#low-complexity 118-164, >POLY_A*simple_repeat
Seq primer: M13 Forward
POLYA=yes

FEATURES

SOURCE

Location/Qualifiers
1. 653
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-D21-cne-a-18-0-U"
/tissue="Chondrosarcoma"
/dev_stage="37 days"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Spine; Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; UI-R-D21 is a normalized cDNA library containing the following tissue(s): Swarm Rat Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pUT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the CATCTGTGA. The Rat cartilaginous tumor tissue was provided by Dr Jeff Stevens at the University of Iowa.
TAG-LIB=UI-R-D21
TAG-TISSUE=cartilaginous tumor
TAG-SEQ=CATCTGTGA"

BASE COUNT 134 a 137 c 137 g 245 t
ORIGIN
Query Match 81.1%; Score 437; DB 14; Length 653;
Best Local Similarity 97.6%; Pred. No. 1,9e-110;
Matches 454; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

67 TTTTACTTCAACAAGCCACAGTGTATGCTCCAGCATTTGGAGGCGACACAGCGGC 126
|||||
653 TTTTACTTCAACAAGCCACAGGCTATGCTCCAGCATTTGGAGGCGACACAGCGGC 594
127 ATTGTGATAGTGTGCTCCGAGGTGATCTGAGGAGGTGGAGATGATCTGTGTC 186
|||||
593 ATTGTGATAGTGTGCTCCGAGGTGATCTGAGGAGGTGGAGATGATCTGTGTC 535
|||||
187 CGGTGACAGCTTACAAAGTACGCTGTTCCATCCGGGCCAGGCCACATGACATGCC 246
|||||
534 CCGGTGACAGCTTACAAAGTACGCTGTTCCATCCGGGCCAGGCCACATGACATGCC 475
247 AAGCTGAGAGTGTGCTCCGAGGTGATCTGAGGAGGTGGAGATGATCTGTGTC 306
|||||
474 AAGCTGAGAGTGTGCTCCGAGGTGATCTGAGGAGGTGGAGATGATCTGTGTC 415
|||||
307 AAAGGAAGTACACTTGAAGAACAACAAGTAGAGAGTGCAGAAAGACTTACAGAA 366
|||||
414 AAAGGAAGTACACTTGAAGAACAACAAGTAGAGAGTGCAGAAAGACTTACAGAA 355
|||||
367 GTAGAGAGAGGCTCCGAGGACAGAAATGACACGTCACCGCAGATCTTGTGCTGT 426

|||||
Db 354 GTAGAGAGAGGCTCCGAGGACAGAAATGCGACGTGCCAGCATCTTGTGCTT 295
QY 427 GAGCAACTGCTCAAAACATCGGAACACCTGCGCAATATCATATAGTTCAATTCAT 486
|||||
Db 294 GAGCAACTGCTCAAAACATCGGAACACCTGCGCAATATCATATAGTTCAATTCAT 235
QY 487 CGAGATGGGCAATTCCTCATGAAATACAGAAATTCATTC 531
|||||
Db 234 CGAGATGGGCAATTCCTCATGAAATACAGAAATTCATTC 190

RESULT 7
BF383724
LOCUS
DEFINITION
602044632F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4194295 5',
mRNA sequence.
BF383724
BF383724.1 GI:11365029
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L19A9527 row: p column: 08
High quality sequence stop: 589.
Location/Qualifiers
1. 594

FEATURES

SOURCE

Location/Qualifiers
1. 594
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4194295"
/clone_lib="NCI_CGAP_L19"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t
ORIGIN
Query Match 80.1%; Score 431.8; DB 12; Length 594;
Best Local Similarity 92.4%; Pred. No. 5e-109;
Matches 465; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

1 GGACAGACACCCCTTTCGGGGCTAGCTGTGAGACGCTTCATGCTGTGTGGACCA 60
|||||
93 GGACAGACACCCCTTTCGGGGCTAGCTGTGAGACGCTTCATGCTGTGTGGACCG 151
61 AGGGGCTTTTACTTCAACAAGCCACAGCTGTGCTCCAGATTCGAGGCGACACAG 120
|||||
152 AGGGGCTTTTACTTCAACAAGCCACAGCTGTGCTCCAGATTCGAGGCGACACAG 211
|||||
QY 121 AGGGGCTTTTACTTCAACAAGCCACAGCTGTGCTCCAGATTCGAGGCGACACAG 180
|||||
Db 212 ACAGGATTTGTGATGAGAGTGTGCTCCGAGCTGTGATCTGAGAGAGTGAAGTATC 271
|||||
QY 181 TGTGTCCGCTGCAAGCTTCAAAAGTACGCTGTTCCATTCGGGCCACAGCCTAGC 240
|||||
Db 272 TGTGCCCACTGCAAGCTTCAAAAGTACGCTGTTCCATTCGGGCCACAGCCTAGC 331

96 a 112 c 124 g 177 t

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UT-M-BH3-ay-g-11-0-01"
/clone_11b="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/label="Vector: pT73D-Pac (Pharmacia)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI. The
NIH_BMAP_M_S4 library is a subtracted library of a series
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR-amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3 ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC

```

	QY	290	AGCTGCAAGAAGAGAAAGGAAGTACACTGTGAAGAACACAAGTAAGAGAAATGCACGA	349
	DB	259	AGCTGCAAGAAGAGAAAGGAAGTACACTGTGAAGAACACAAGTAAGAGAAATGCACGA	200
	QY	350	AACACAGCCTTCACGATGTGTAGGAGAGACCCTCCGAGAGAACAGAAAATGCCAGTCA	409
	DB	199	AACAGAGCCCTCACAAATGTGTAGGAGAGACCCTCCGAGAGAACAGAAAATGCCAGTCA	140
	QY	410	AAGATCGCTTTGCGCTTGAGCAACCTGCAACAAACATGGGAACACCTGGCCAATATCAATA	469
	DB	139	AGGATTCCTTTGCTGCTTGAGCAACCTGCAACAAACATGGGAACACCTGGCCAATATCAATA	80
	QY	470	TGAGTTCATATCATCTTTCAGAGATGGGCATTTCCTCCATGAAATACACAGATAA	529
	DB	79	TAAATCCAAATACATATCAAAAGATGGGACATTCCCAATGAATATATCAAGTAACATT	20
	QY	530	CCCCGAA	536
	DB	19	CCAAAA	13
RESULT 10 A1876493/c				
LOCUS				
DEFINITION				
u159db10.xl Sugano mouse liver b1a Mus musculus CDNA clone				
IMAGE:1924219.3 similar to gb:AF57025.fna1 INSULIN-LIKE GROWTH				
FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for				
proinsulin-like growth factor IB (MOUSE); mRNA sequence.				
A1876493				
A1876493.1 GI:5550542				
EST.				
house mouse.				
Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
1 (bases 1 to 642)				
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,				
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person				
,B., Swaller,T., Gibbons,M., Page,D., Harrey,N., Schurk,R., Ritter				
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,				
Waterston,R. and Wilson,R.				
The WashU-NCI Mouse EST Project 1999				
Unpublished (1999)				
Contact: Marra M/WashU-NCI Mouse EST Project 1999				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
Tel.: 314 286 1800				
Fax: 314 286 1810				
Email: mouseest@wustl.edu				
This clone is available royalty-free through LNLN ; contact the				
IMAGE Consortium (infoimage.llnl.gov) for further information.				
MGI:980511				
Seq primer: custom primer used				
High quality sequence stop: 257.				
FEATURES				
Source				
1..642				
Location/Qualifiers				
1..642				
/organism="Mus musculus"				
/strain="C57BL"				
/db_xref="taxon:10090"				
/clone="IMAGE:1924219"				
/clone_1bp="Sugano mouse liver b1a"				
/sex="female"				
/dev_stage="adult"				
/lab_host="DH10B"				
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII				
(CACTGTG); Site_2: DraII (CAGCATG); 1st strand cDNA				
[ATGAGCCCTTTTTTTTTTTTTT]; double-stranded cDNA was				
ligated to a DraIII adaptor [TTGtgacctctg], digested				
and cloned into distinct DraIII sites of the pME18S-FL3				
vector ('5' site CACTGTG, 3' site CAGCATG). XhoI should				
be used to isolate the cDNA insert. Site selection was				

performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTCTCTTAAGTGGG and 3' end primer CGACCTGCAGCTCGACCA.

BASE COUNT 127 a 154 c 175 g 185 t 1 others

Query Match 78.1%; Score 421.2; DB 9; Length 642;
Best Local Similarity 91.1%; Pred. No. 4.5e-106;
Matches 458; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Y 2 GACCAAGACCTTTCCGGGCTGAGCTGTGAGCCTCTTCAAGTTCGTGTGACCA 61
Db 503 GACCAAGACCTTTCCGGGCTGAGCTGTGAGCCTCTTCAAGTTCGTGTGACCA 444
Y 62 GGGGCTTTTACTCACAAGCCACAGTATGGCTCCAGCATTTGGAGGACCAACA 121
Db 443 GGGGCTTTTCTTCAACAAGCCACAGTATGGCTCCAGCATTTGGAGGACCAACA 384
Y 122 CGGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 383 CAGTCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
Y 181 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 240
Db 323 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 264
Y 241 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 300
Db 263 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 204
Y 301 AAGAAGAAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 360
Db 203 AAGAAGAAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 144
Y 361 CAGAATGTAGAGAGAGCTCCGAGGACAGAAATGCCAGTCAAGTCAAGTCAAG 420
Db 143 CAGAATGTAGAGAGAGCTCCGAGGACAGAAATGCCAGTCAAGTCAAGTCAAG 84
Y 421 CTGCTTGAACAACCTGCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 480
Db 83 CTGCTTGAACAACCTGCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 24
Y 481 TCATTTCAGAGATGGGCAATTTC 503
Db 23 ACATTTCAGAGATGGGCAATTTC 1

RESULT 11 525 bp mRNA linear EST 09-MAR-1999
AA963258
LOCUS UI-R-El-9h-f-04-0-UI.s1 UI-R-El Rattus norvegicus cDNA clone
DEFINITION UI-R-El-9h-f-04-0-UI 3', mRNA sequence.

ACCESSION AA963258
VERSION AA963258.1 GI:4278182
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 525)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On May 18, 1998 this sequence version replaced gi:3136750.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.iowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult 12-day-embryo library. cDNA library preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics
Seq primer: M13 Forward
Location/Qualifiers
1. 525

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-El-9h-f-04-0-UI"
/clone_1bp="UI-R-El"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-El
library is a subtracted library derived from the UI-R-El
library. The UI-R-El library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-El) was constructed as follows: PCR
amplified cDNA inserts from a pool of UI-R-El clones from
which 3' ESTs had been derived was used as a driver in a
hybridization with the UI-R-El library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-El
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996).

BASE COUNT 107 a 133 c 126 g 159 t

Query Match 74.7%; Score 402.6; DB 9; Length 525;
Best Local Similarity 88.5%; Pred. No. 6e-101;
Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;

Y 1 GGACCAAGACCTTTCCGGGCTGAGCTGTGAGCCTCTTCAAGTTCGTGTGACCA 60
Db 521 GGACCAAGACCTTTCCGGGCTGAGCTGTGAGCCTCTTCAAGTTCGTGTGACCA 462
Y 61 AGGGCTTTTACTCACAAGCCACAGTATGGCTCCAGCATTTGGAGGACCAACA 120
Db 461 AGGGCTTTTACTCACAAGCCACAGTATGGCTCCAGCATTTGGAGGACCAACA 402
Y 121 ACGGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 401 ACGGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
Y 181 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 240
Db 341 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 282
Y 241 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 300
Db 281 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 267
Y 301 AAGAAGAAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 360
Db 266 -----AAGAAGTACACTTGAAGACACAGTAGAGAAAGTCCAGAAACAGACTA 214
Y 361 CAGAATGTAGAGAGAGCTCCGAGGACAGAAATGCCAGTCAAGTCAAGTCAAGTCA 420
Db 213 CAGAATGTAGAGAGAGCTCCGAGGACAGAAATGCCAGTCAAGTCAAGTCAAGTCA 154

QY 421 CTGCTTGACCACTGCAAAACATGGAACCTGCCAAATATCATATAGATTCAATA 480
 |||
 Db 153 CTGCTTGACCACTGCAAAACATGGAACCTGCCAAATATCATATAGATTCAATA 94
 |||
 QY 481 TCATTTGAGAGATGGGCACTTTCCCTCAATGAATAACAGATAAATCAATTC 531
 |||
 Db 93 CCATTTGAGAGATGGGCACTTTCCCTCAATGAATAACAGATAAATCAATTC 43
 |||

RESULT 12
 AA945553 500 bp mRNA linear EST 08-JAN-1999
 LOCUS EST01052 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
 DEFINITION RL1083 3' end, mRNA sequence.
 ACCESSION AA945553
 VERSION AA945553.1 GI:4132547
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 500)
 Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Keriavage,A.R. and Adams,M.D.
 Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
 Gene Index
 Unpublished (1998)
 On May 1, 1998 this sequence version replaced gi:3105465.
 CONTACT: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.

FEATURES
 Location/Qualifiers
 1..500
 /organism="Rattus sp."
 /db_xref="taxon:10118"
 /clone="RL1083"
 /dev_stage="embryo 8, 12, 18 dpc"
 /note="Organ: liver; Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"
 BASE COUNT 99 a 125 c 130 g 142 t
 ORIGIN

Query Match 74.5%; Score 401.6; DB 9; Length 500;
 Best Local Similarity 88.5%; Pred. No. 1,1e-100;
 Matches 469; Conservative 0; Mismatches 9; Indels 52; Gaps 1;

QY 1 GGACCAAGAGACCCCTTGGGGGCTGAGCTGGTGAGCACTCTTCAGTTCGTGTGACCA 60
 |||
 Db 478 GGACCAAGAGACCCCTTGGGGGCTGAGCTGGTGAGCACTCTTCAGTTCGTGTGACCA 419
 |||
 QY 61 AGGGGCTTTTACTCTCAACAAGCCACAGTCTATGGCTCCAGCARTCGGAGGCAACCAG 120
 |||
 Db 418 AGGGGCTTTTACTCTCAACAAGCCACAGTCTATGGCTCCAGCARTCGGAGGCAACCAG 359
 |||
 QY 121 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGTAC 180
 |||
 Db 358 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGTAC 299
 |||
 QY 181 TGTGTCCGCTGCAAGCCTACAAATGCTGCTTCATCCGGGCGCAGCCCACTGAC 240
 |||
 Db 298 TGTGTCCGCTGCAAGCCTACAAATGCTGCTTCATCCGGGCGCAGCCCACTGAC 239
 |||
 QY 241 ATGCCCAAGACTCAGAAGTCCAGCCCTATCGACACACAAGAAAGAGAGTGCAGAGG 300
 |||
 Db 238 ATGCCCAAGACTCAG----- 224
 |||
 QY 301 AGAAGAAAGAGAGTACACTTGAAGAACAAGTAGAGAGAGTGCAGAGAAACAAGACTTA 360
 |||

Db 223 -----AAGCACTTACACTTGAAGAACAAGTAGAGAGAGTGCAGAGAAACAAGACTTA 171
 |||
 QY 361 CAGATGTAGAGAGAGGCTCCCGAGAACAGAAATGCCAGCTCCAGCAAGATCTTTG 420
 |||
 Db 170 CAGATGTAGAGAGAGGCTCCCGAGAACAGAAATGCCAGCTCCAGCAAGATCTTTG 111
 |||
 QY 421 CTGCTTGAGCAACCTGCAAAACATCGGACACCTGCCAAATATCATATAGATTCAATA 480
 |||
 Db 110 CTGCTTGAGCAACCTGCAAAACATCGGACACCTGCCAAATATCATATAGATTCAATA 51
 |||

QY 481 TCATTTGAGAGATGGGCACTTTCCCTCAATGAATAACAGATAAATCAATTC 530
 |||
 Db 50 CCATTTGAGAGATGGGCACTTTCCCTCAATGAATAACAGATAAATCAATTC 1
 |||

RESULT 13
 A1599751 525 bp mRNA linear EST 21-APR-1999
 LOCUS EST251454 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
 DEFINITION REME86 3' end, mRNA sequence.
 ACCESSION A1599751
 VERSION A1599751.1 GI:4608799
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 525)
 Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Keriavage,A.R. and Adams,M.D.
 Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
 Gene Index
 Unpublished (1998)
 CONTACT: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.

FEATURES
 Location/Qualifiers
 1..525
 /organism="Rattus sp."
 /db_xref="taxon:10118"
 /clone="REME86"
 /dev_stage="embryo 8, 12, 18 dpc"
 /note="Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"
 BASE COUNT 107 a 133 c 140 g 145 t
 ORIGIN

Query Match 74.1%; Score 399.4; DB 9; Length 525;
 Best Local Similarity 88.1%; Pred. No. 4.7e-100;
 Matches 468; Conservative 0; Mismatches 11; Indels 52; Gaps 1;

QY 1 GGACCAAGAGACCCCTTGGGGGCTGAGCTGGTGAGCACTCTTCAGTTCGTGTGACCA 60
 |||
 Db 480 GGACCAAGAGACCCCTTGGGGGCTGAGCTGGTGAGCACTCTTCAGTTCGTGTGACCA 421
 |||
 QY 61 AGGGGCTTTTACTCTCAACAAGCCACAGTCTATGGCTCCAGCARTCGGAGGCAACCAG 120
 |||
 Db 420 AGGGGCTTTTACTCTCAACAAGCCACAGTCTATGGCTCCAGCARTCGGAGGCAACCAG 361
 |||
 QY 121 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGTAC 180
 |||
 Db 360 ACGGCAATTTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGTAC 301
 |||
 QY 181 TGTGTCCGCTGCAAGCCTACAAATGCTGCTTCATCCGGGCGCAGCCCACTGAC 240
 |||
 Db 300 TGTGTCCGCTGCAAGCCTACAAATGCTGCTTCATCCGGGCGCAGCCCACTGAC 241
 |||

QY 241 ATGCCAGAGCTCAGAGTCCCGCCCTATCGACACAGAGAAAAGAGCTGCAAGG 300
 |||||||
 Db 240 ATGCCAGAGCTCAG----- 226
 QY 301 AGAGAGAAAGAGTACCTTAAGAGACAGAGTAGAGAGAGTGCAGAAACAGACCTA 360
 |||||||
 Db 225 -----AAGGAGAGTACCTTAAGAGACAGAGTAGAGAGAGTGCAGAAACAGACCTA 173
 QY 361 CAGATGTAGAGAGAGCCCTCCGAGAGAGAGAAATGCCAGCTACCCGAAATGCTTTG 420
 |||||||
 Db 172 CAGAGATGTAGAGAGAGCCCTCCGAGAGAGAGAGAAATGCCAGCTACCCGAAATGCTTTG 113
 QY 421 CTGCTTGAGCAACCTGCAGAAACATCGAGACACCTGCCAAATATCAATATGAGTTCAATA 480
 |||||||
 Db 112 CTGCTTGAGCAACCTGCAGAAACATCGAGACACCTGCCAAATATCAATATGAGTTCAATA 53
 QY 481 TCATTTCAGAGATGGGCTATTCCTCAATGAATACAGAGTAACATTCC 531
 |||||||
 Db 52 CCATTTCAGAGATGGGCTATTCCTCAATGAATACAGAGTAACATTCC 2

RESULT 14
 BI294072/c 499 bp mRNA linear EST 19-JUL-2001
 LOCUS UI-R-DK0-cej-b-03-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
 DEFINITION UI-R-DK0-cej-b-03-0-UI 3', mRNA sequence.
 ACCESSION BI294072
 VERSION BI294072.1 GI:14956179
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 499)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dt track served to identify it as a clone from the
 normalized rat heart pool library cDNA library preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES

Source Location/Qualifiers
 1..499
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-DK0-cej-b-03-0-UI"
 /clone_lib="UI-R-DK0"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pUT33-Pac (Pharmacia) with a modified
 polylinker. Site1: Not I; Site2: Eco RI; The UI-R-DK0
 library is a subtracted library derived from a mixture of
 five individually tagged normalized rat libraries:
 brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%),
 aorta-nRBP (20%), and placenta-nRBP (20%). Each original
 library was constructed from a mixture of equal amounts of

RNA from seven different developmental time-points:
 embryonic day 17, embryonic day 19, embryonic day 21,
 adult day 1, adult day 12, adult day 75, and adult day
 200. (Exception: the aorta pool does not contain embryonic
 day 17 RNA and the placenta pool contains only the three
 embryonic stages). Each library was normalized
 individually according to the procedure described by
 Bonaldo, Lennon & Soares (Genome Research 6:
 791-806, 1996). For construction of the DK0 subtracted
 library, plasmid DNA from each of the five individually
 tagged, normalized libraries was mixed in the proportions
 specified above and electroporated into competent bacteria
 for production of single-stranded circular DNA
 representing the pool of libraries. Single-stranded
 circular DNA representing these five normalized libraries
 was then used as a tracer in a subtractive hybridization
 with a driver (PCR amplified inserts from a plasmid DNA
 template preparation) comprising: a) a set of about 1,000
 arrayed clones from each of the five non-normalized
 libraries of brain (C70s), heart (C50s), kidney (C90s),
 aorta (C90s), and placenta (C90s). The resulting pool of
 approximately 5,000 clones represented about 33.3% of the
 final driver population. A set of about 2,000 arrayed
 clones from each of the five normalized libraries of brain
 (C70), heart (C50), kidney (C90), aorta (C90), and
 placenta (C90). The resulting pool of about 10,000 clones
 represented about 66.6% of the final driver population.
 TAG-LIB-UI-R-DK0
 TAG-TISSUE-rat heart pool
 TAG_SEQ-ATAAGTATAC"

BASE COUNT 97 a 124 c 121 g 156 t 1 others
 ORIGIN
 Query Match 73.3%; Score 395; DB 13; Length 499;
 Best Local Similarity 88.0%; Pred. No. 7.6e-99;
 Matches 463; Conservative 0; Mismatches 11; Indels 52; Gaps 1;
 QY 6 AGAGACCTTTGGGGGCTGAGCTGTGAGAGCTCTTCACTGTGTGTGAGCAAGGG 65
 |||||||
 Db 499 AGAGACCTTTGGGGGCTGAGCTGTGAGAGCTCTTCACTGTGTGTGAGCAAGGG 440
 QY 66 CTCTTACTTAAACAGGCCACAGTCATGAGCTCAGATTCGGAGGACACAGACGGG 125
 |||||||
 Db 439 CTCTTACTTAAACAGGCCACAGTCATGAGCTCAGATTCGGAGGACACAGACGGG 380
 QY 126 CATTTGATGATGTTGCTTCGGAGCTGTGATCTGAGAGGCTGAGATGACTGTG 185
 |||||||
 Db 379 CATTTGATGATGTTGCTTCGGAGCTGTGATCTGAGAGGCTGAGATGACTGTG 320
 QY 186 CCGCTGAGAGCTTACAGAGTACAGTCTGCTCCAGCGCCGACGACACTACATGCC 245
 |||||||
 Db 319 TCCGCTTAAAGCTTACAGAGTACAGTCTGCTCCAGCGCCGACGACACTACATGCC 260
 QY 246 CAAGACTCAGAGTCCAGGCCCTATCGACACAGAAAAGGAAGACTGTGAAAGGAGAG 305
 |||||||
 Db 259 CAAGACTCAG----- 250
 QY 306 GAAGAGAGTACACTTGAAGACACAGAGTAGAGAGTAGAGAGAGAGAGAGAGAG 365
 |||||||
 Db 249 --AAGGAGAGTACACTTGAAGACACAGAGTAGAGAGTAGAGAGAGAGAGAGAG 192
 QY 366 TGTAGAGAGAGCTCCCGAGAGACAGAAATGCGAGTCCAGCCAGAGTCTTGTGCT 425
 |||||||
 Db 191 TGTAGAGAGAGCTCCCGAGAGAGAGAAATGCGAGTCCAGCCAGAGTCTTGTGCT 132
 QY 426 TGAGCAACCTGCAGAAATGAGAGACCTGCCAAATATCAATATGAGTTCAATATTC 485
 |||||||
 Db 131 TGAGCAACCTGCAGAAATGAGAGACCTGCCAAATATCAATATGAGTTCAATATTC 72
 QY 486 TCAGAGATGGGCAATTTCCCTCAATGAATACAGAGTAACATTCC 531
 |||||||
 Db 71 TCAGAGATGGGCAATTTCCCTCAATGAATACAGAGTAACATTCC 26

RESULT 15
LOCUS A1104669/c 502 bp mRNA linear EST 08-JAN-1999
DEFINITION EST21938 Normalized rat heart, Bento Soares Rattus sp. cDNA clone.
RHECH40 3' end, mRNA sequence.
ACCESSION A1104669
VERSION A1104669.1 GI:4134279
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 502)
Lee, N.H., Glodde, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R., and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
Unpublished (1998)
On Oct 6, 1998 this sequence version replaced gi:3708981.
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..502
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RHECH40"
/clone_1id="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT733pac; site_1: EcoRI;
site_2: NotI"
BASE COUNT 108 a 128 c 122 g 144 t
ORIGIN
Query Match 73.1%; Score 394.2; DB 9; Length 502;
Best Local Similarity 87.7%; Pred. No. 1.3e-98;
Matches 464; Conservative 0; Mismatches 13; Indels 52; Gaps 1;
QY 3 ACCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGTGACCAAG 62
DB 502 ACCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGTGACCAAG 443
QY 63 GGGCTTTACTTCAACAGCCACAGCTCTATGCTCCAGCATTCGAGGGGACACACAGAC 122
DB 442 GGGTTTACTTCAACAGCCACAGCTCTATGCTCCAGCATTCGAGGGGACACACAGAC 383
QY 123 GGGCATTTGTGAGTGTGCTTCCGAGACTGTGATCTGAGGAGGCTGGAGTGTACTG 182
DB 382 GGGCATTTGTGAGTGTGCTTCCGAGACTGTGATCTGAGGAGGCTGGAGTGTACTG 323
QY 183 TGTCCGCTGCAAGCTACAAAGTCACTGCTTCATCCGGCCGACGACACAGTACAT 242
DB 322 TGCTCCGCTGCAAGCTACAAAGTCACTGCTTCATCCGGCCGACGACACAGTACAT 263
QY 243 GCCCAAGACTCAGAGTCCAGCCCTATCGACACACAAGAAAGAGAGCTGCAAGAGAG 302
DB 262 GCCCAAGACTCAG----- 250
QY 303 AAGGAAGAGAGTACACTGGAAGACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 362
DB 249 -----AAGGAAGAGAGTACACTGGAAGACAGTACAGTACAGTACAGTACAGTACAGTAC 195
QY 363 GAATGTAAGAGAGCTCCGAGAGAAAGAAATGCCACGTACCCGCAAGATCTTTGCT 422
DB 194 GAATGTAAGAGAGCTCCGAGAGAAAGAAATGCCACGTACCCGCAAGATCTTTGCT 135
QY 423 GCTTGACCACTGCAGAAACATGGAACACCTGCCAAATATCAATATGATGATTCAATATC 482
DB 134 GCTTGACCACTGCAGAAACATGGAACACCTGCCAAATATCAATATGATGATTCAATATC 75

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